

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 18:39:31 ; Search time 158 Seconds
(without alignments)
862.767 Million cell updates/sec

Title: US-10-676-358-1
Perfect score: 2085
Sequence: 1 EFPFKYLVDETSHTQLLC.....QKLFLEWGNQGVKISCL 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:.*
1: geneseqp1980s.*
2: geneseqp1930s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2085	100.0	380	4 AAB66988	Murine OP
2	2085	100.0	380	8 ADM28827	Human ost
3	2085	100.0	381	8 ADM28870	Human OP
4	2085	100.0	382	8 ADM28869	Human OP
5	2085	100.0	385	8 ADM28876	Human OP
6	2085	100.0	391	8 ADM28877	Human OP
7	2085	100.0	400	6 ABU08820	Human ost
8	2085	100.0	401	2 ABW38345	Human ost
9	2085	100.0	401	3 AAY43400	Osteoprot
10	2085	100.0	401	4 AAB66976	Human OP
11	2085	100.0	401	5 ABG71823	Wild type
12	2085	100.0	401	6 ABP55109	Human ost
13	2085	100.0	401	6 AAB34363	Human ost
14	2085	100.0	401	7 AD01627	Human ost
15	2085	100.0	401	8 ADM28813	Human ost
16	2085	100.0	537	6 AAO19639	Human mil
17	2080	99.8	401	5 ABG73895	Human OP
18	2080	99.8	401	5 ABG73894	Human OP
19	2079	99.7	380	2 AAR99924	Mature os
20	2079	99.7	380	6 AAO19638	Human mil
21	2079	99.7	380	7 ADF15245	Human alb
22	2079	99.7	380	8 ADM28860	Human ost
23	2079	99.7	391	2 AAW53238	Human OCI
24	2079	99.7	401	2 AAR99925	Full leng
25	2079	99.7	401	2 AAW53239	Human OCI

ALIGNMENTS

RESULT 1

AAB66988
ID AAB66988 standard; protein; 380 AA.

XX AAB66988;

XX 19-APR-2001 (first entry)

XX Murine OPG cysteine-rich domain.

DE Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
KW ischaemia; Parkinson's disease.

XX Mus sp.

XX WO200103719-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-US018667.

XX 09-JUL-1999; 99US-00350670.

XX 09-DEC-1999; 99US-00457647.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX WPI; 2001-103031/11.

XX Treating conditions leading to bone loss such as rheumatoid arthritis,
XX multiple sclerosis and asthma, comprises administering an osteoprotegerin
XX protein in conjunction with e.g. inhibitors of interleukin and tumor
XX necrosis factor alpha.

XX Disclosure; Fig 12; 316pp; English.

XX The present invention relates to a method for treating conditions leading
XX to bone loss. The method comprises administering a purified and isolated
XX osteoprotegerin (OPG) protein (AA057836-AA057838 and AAB66974-AAB66976)
XX in conjunction with other substances such as tumour necrosis factor-alpha
XX (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, IGF
XX modulators, fibroblast growth factor (FGF) 1-10 modulators and/or platelet

Aay05742 Tumour ne
Aaw5030 Tumour ne
Aaw83926 Human FTH
Aay88622 Osteoclas
Aab18715 A human t
Aab60570 Human TNF
Abg73893 Human OPG
Aae36245 Human TRA
Aao31135 Human TRA
Abp70997 Human ost
Add01625 Human ost
Add37427 Human ost
Adf16158 Human alb
Adf16153 Human alb
Adf16151 Human alb
Adf15231 Human alb
Adf16152 Human alb
Adf16154 Human alb
Adf16155 Human alb
Adf16156 Human alb

activating factor (PAP) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock

XX SQ Sequence 380 AA;

Query Match 100.0%; Score 2085; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.2e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCHTAKWKIVCAPDPHYTDSWHTSDECL 60
Db 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCHTAKWKIVCAPDPHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQKQECNTHNRVCECKGKRYLEIFCLKHSRCPGFGVVQAGTPERNTV 120
Db 61 YCSPVCKELQYVQKQECNTHNRVCECKGKRYLEIFCLKHSRCPGFGVVQAGTPERNTV 120
QY 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICGNSSESTOKCGIDVTL 180
Db 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICGNSSESTOKCGIDVTL 180
QY 181 CEAEFRFAVPTKFTPNWLSVLVNLPGTKVNAESVERIKROHSQEQFTQLLKLWKHQN 240
Db 181 CEAEFRFAVPTKFTPNWLSVLVNLPGTKVNAESVERIKROHSQEQFTQLLKLWKHQN 240
QY 241 KAQDIVKLLIQQIDICLNSVQRHIGHANLTFEQLSLMESLPKKGVAEDIEKTKACKP 300
Db 241 KAQDIVKLLIQQIDICLNSVQRHIGHANLTFEQLSLMESLPKKGVAEDIEKTKACKP 300
QY 301 SQIILKLLSLWRKNGDQDTLXGLMHALKSKTYHFPKTVTQSLKKTIRFLHSFTWKLY 360
Db 301 SQIILKLLSLWRKNGDQDTLXGLMHALKSKTYHFPKTVTQSLKKTIRFLHSFTWKLY 360
QY 361 QKLFLEVMIGNOVQSVKISCL 380
Db 361 QKLFLEVMIGNOVQSVKISCL 380

RESULT 2

ADM28827

ID ADM28827 standard; protein; 380 AA.

XX ADM28827;

AC ADM28827;

DT 20-MAY-2004 (first entry)

XX Human osteoprotegerin cysteine-rich domains 1-4 plus C-terminus #1.

XX Mouse; OPG; bone resorption; excessive bone loss; osteoporosis;
KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
KW Riley-day syndrome; immobilisation of extremity; tumour;
KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
KW osteoprotegerin; transgenic.

XX Mus sp.

XX US2003207827-A1.

XX 06-NOV-2003.

XX 24-SEP-1999; 99US-00405032.

XX 22-DEC-1995; 95US-00577788.
PR 03-SEP-1996; 96US-00706945.
PR 20-DEC-1996; 96US-00771777.
PR 12-AUG-1998; 98US-00132985.
XX (BOYL/) BOYLE W J.
PA (LACEY/) LACEY D L.
PA (CALZ/) CALZONE F J.
PA (CHAN/) CHANG M.

XX Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX WPI; 2004-041572/04.

XX Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis.

XX Disclosure; SEQ ID NO 139; 141pp; English.

XX The invention relates to a purified and isolated polypeptide having osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or having amino terminus at residue 22, and 1-216 amino acids are deleted from carboxy terminus of human OPG polypeptide. Also included are an isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression vector comprising OPG NA, a host cell transformed or transfected with the vector, a transgenic mammal comprising the cell, producing OPG, a polypeptide comprising an amino acid sequence of at least about 164 amino acids comprising four cysteine-rich domains characteristic of the cysteine rich domains of tumour necrosis factor receptor extracellular regions (and an activity of increasing bone density), an antibody (Ab) or its fragment which specifically binds to OPG, a composition comprising OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) and an osteoprotegerin multimer consisting of osteoprotegerin monomers. Ab is useful for detecting the presence of OPG in a biological sample which involves incubating the sample with Ab under conditions that allow binding of ab to OPG and detecting the bound Ab. OPG is useful for assessing the ability of a candidate substance to bind to OPG. OPG NA is useful for regulating the levels of OPG in an animal (human). The nucleic acid promotes an increasing in tissue level of OPG. OPG is useful for treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to osteomyelitis, osteolytic metastasis, and periodontal bone loss. The method further involves administering a substance chosen from bone morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1 inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues, parathyroid hormone related protein and their analogues, E series of prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is useful for treating osteoporosis such as primary osteoporosis, endocrine osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta, homocystinuria, Menke's syndrome, and Riley-day syndrome) and osteoporosis due to immobilisation of extremities, hypercalcaemia resulting from solid tumours and haematologic malignancies (multiple myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with hyperthyroidism and renal function disorders, osteopaenia following surgery and osteonecrosis or bone cell death. The present sequences is an OPG protein (or fragment).

XX SQ Sequence 380 AA;

Query Match 100.0%; Score 2085; DB 8; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.2e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCHTAKWKIVCAPDPHYTDSWHTSDECL 60
Db 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCHTAKWKIVCAPDPHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQKQECNTHNRVCECKGKRYLEIFCLKHSRCPGFGVVQAGTPERNTV 120

Db 61 YCSPVCKELQYVQKQCNTRTHRVCECKEGRYLEIEFCLKHSRCPGGVVOAGTPERNTV 120
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTLL 180
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTLL 180
 QY 181 CEEAFRFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKRQHSOBTQFOLLKWKHQN 240
 Db 181 CEEAFRFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKRQHSOBTQFOLLKWKHQN 240
 QY 241 KAQDIKKIQQIDILCENSQRHIGHANLTFEQLRSIMESLPGKKGVAEDIEKTIKACP 300
 Db 241 KAQDIKKIQQIDILCENSQRHIGHANLTFEQLRSIMESLPGKKGVAEDIEKTIKACP 300
 QY 301 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 360
 Db 301 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 360
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 361 QKLFLEMIGNQVQSVKISCL 380
 RESULT 3
 ADM28870
 ID ADM28870 standard; protein; 381 AA.
 XX
 AC ADM28870;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human OPG truncation mutant, OPG met[22-401].
 XX
 KW Human; OPG; bone resorption; excessive bone loss; osteoporosis;
 KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
 KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
 KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
 KW Riley-day syndrome; immobilisation of extremity; tumour;
 KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
 KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
 KW osteoprotegerin; transgenic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2003207827-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 24-SEP-1999; 99US-00405032.
 XX
 PR 22-DEC-1995; 95US-00577788.
 PR 03-SEP-1996; 96US-00706945.
 PR 20-DEC-1996; 96US-00771777.
 PR 12-AUG-1998; 98US-00132985.
 XX
 PA (BOYLE/) BOYLE W J.
 PA (LACE/) LACEY D L.
 PA (CALZ/) CALZONE F J.
 PA (CHAN/) CHANG M.
 XX
 FI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
 XX WPI; 2004-041572/04.
 DR
 XX Novel osteoprotegerin useful for treating conditions resulting in bone
 PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
 PT loss caused by rheumatoid arthritis or osteomyelitis.
 XX
 PS Claim 37; Page; 141pp; English.
 XX
 CC The invention relates to a purified and isolated polypeptide having

CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
 CC having amino terminus at residue 22, and 1-216 amino acids are deleted
 CC from carboxy terminus of human OPG polypeptide. Also included are an
 CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
 CC vector comprising OPG NA, a host cell transformed or transfected with the
 CC polypeptide comprising an amino acid sequence of at least about 164 amino
 CC acids comprising four cysteine-rich domains characteristic of the
 CC cysteine rich domains of tumour necrosis factor receptor extracellular
 CC regions (and an activity of increasing bone density), an antibody (Ab) or
 CC its fragment which specifically binds to OPG, a composition comprising
 CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
 CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
 CC Ab is useful for detecting the presence of OPG in a biological sample
 CC which involves incubating the sample with Ab under conditions that allow
 CC binding of Ab to OPG and detecting the bound Ab. OPG is useful for
 CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
 CC useful for regulating the levels of OPG in an animal (human). The nucleic
 CC acid promotes an increasing in tissue level of OPG. OPG is useful for
 CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
 CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
 CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
 CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
 CC method further involves administering a substance chosen from bone
 CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
 CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
 CC parathyroid hormone related protein and their analogues, E series of
 CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
 CC useful for treating osteoporosis such as primary osteoporosis, endocrine
 CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
 CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
 CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
 CC osteoporosis due to immobilisation of extremities, hypercalcaemia
 CC resulting from solid tumours and haematologic malignancies (multiple
 CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
 CC hypercalcaemia associated with hyperthyroidism and renal function
 CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
 CC death. The present sequences is an OPG truncation/deletion or
 CC substitution mutant protein (or fragment).
 XX
 SQ Sequence 381 AA;

Query Match 100.0%; Score 2085; DB 8; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5.2e-153;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ETTPPKYLHYDEETSHQLLCDKCPGGHYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 60
 Db 2 ETTPPKYLHYDEETSHQLLCDKCPGGHYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 61
 QY 61 YCSPVCKELQVVKQECNTRTHRVCECKEGRYLEIEFCLKHSRCPGGVVOAGTPERNTV 120
 Db 62 YCSPVCKELQVVKQECNTRTHRVCECKEGRYLEIEFCLKHSRCPGGVVOAGTPERNTV 121
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTLL 180
 Db 122 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTLL 181
 QY 181 CEEAFRFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKRQHSOBTQFOLLKWKHQN 240
 Db 182 CEEAFRFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKRQHSOBTQFOLLKWKHQN 241
 QY 241 KAQDIKKIQQIDILCENSQRHIGHANLTFEQLRSIMESLPGKKGVAEDIEKTIKACP 300
 Db 242 KAQDIKKIQQIDILCENSQRHIGHANLTFEQLRSIMESLPGKKGVAEDIEKTIKACP 301
 QY 301 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 360
 Db 302 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 361
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 362 QKLFLEMIGNQVQSVKISCL 381

RESULT 4
ADM28869
ID ADM28869 standard; protein; 382 AA.
XX
AC ADM28869;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human OPG truncation mutant, OPG met-lys[22-401].
XX
KW Human; OPG; bone resorption; excessive bone loss; osteoporosis;
KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
KW steroid-induced osteopaenia; rheumatoid arthritis; hypercalcaemia;
KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
KW Riley-day syndrome; immobilisation of extremity; tumour;
KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
KW osteoprotegerin; transgenic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN US2003207827-A1.
PD 06-NOV-2003.
XX
PF 24-SEP-1999; 99US-00405032.
XX
FR 22-DEC-1995; 95US-00577788.
PR 03-SEP-1996; 96US-00706945.
PR 20-DEC-1996; 96US-00771777.
PR 12-AUG-1998; 98US-00132985.
XX
PA (BOYLE/) BOYLE W J.
PA (LACEY/) LACEY D L.
PA (CALZ/) CALZONE F J.
PA (CHAN/) CHANG M.
XX
PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
XX
XX WPI; 2004-041572/04.
DR
XX
PT Novel osteoprotegerin useful for treating conditions resulting in bone
PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
PT loss caused by rheumatoid arthritis or osteomyelitis.
XX
PS Claim 37; Page, 14pp; English.
XX
CC The invention relates to a purified and isolated polypeptide having
CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse,
CC having amino terminus at residue 22, and 1-216 amino acids are deleted
CC from carboxy terminus of human OPG polypeptide. Also included are an
CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
CC vector comprising OPG NA, a host cell transformed or transfected with the
CC polypeptide comprising an amino acid sequence of at least about 164 amino
CC acids comprising four cysteine-rich domains characteristic of the
CC cysteine rich domains of tumour necrosis factor receptor extracellular
CC regions (and an activity of increasing bone density), an antibody (Ab) or
CC its fragment which specifically binds to OPG, a composition comprising
CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
CC Ab is useful for detecting the presence of OPG in a biological sample
CC which involves incubating the sample with Ab under conditions that allow
CC binding of Ab to OPG and detecting the bound Ab. OPG is useful for
CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
CC useful for regulating the levels of OPG in an animal (human). The nucleic
CC acid promotes an increasing in tissue level of OPG. OPG is useful for
CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced

osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
method further involves administering a substance chosen from bone
morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
parathyroid hormone related protein and their analogues, E series of
prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
useful for treating osteoporosis such as primary osteoporosis, endocrine
osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
osteoporosis due to immobilisation of extremities, hypercalcaemia
resulting from solid tumours and haematologic malignancies (multiple
myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
hypercalcaemia associated with hyperthyroidism and renal function
disorders, osteopaenia following surgery and osteonecrosis or bone cell
death. The present sequences is an OPG truncation/deletion or
substitution mutant protein (or fragment).

SQ Sequence 382 AA;

Query Match 100.0%; Score 2085; DB 8; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.2e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFFPKYLHYDEETSHQLLCDKCPGTLYLKQCTAKWTKVCAPCDPHYVYDTSWHTSDECL 60
DB 3 ETFFPKYLHYDEETSHQLLCDKCPGTLYLKQCTAKWTKVCAPCDPHYVYDTSWHTSDECL 62
QY 61 YCSPVCKELQYVQECNRTNHRVCKEGRYLEIEFCLKXRCPPFGVGVQAGTPERNTV 120
DB 63 YCSPVCKELQYVQECNRTNHRVCKEGRYLEIEFCLKXRCPPFGVGVQAGTPERNTV 122
QY 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLITQGNATHDNCISGNSESTOKCGIDVTL 180
DB 123 CKRCPDGFNETSSKAPCRKHTNCSVFGLLITQGNATHDNCISGNSESTOKCGIDVTL 182
QY 181 CEEAFFFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQBQTFOLLKLWKHQN 240
DB 183 CEEAFFFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQBQTFOLLKLWKHQN 242
QY 241 KAQDIVKKIIQDILCENSQVRHGHANLTFEQLRSLMESLFGKXVGAEDIEKTKACKP 300
DB 243 KAQDIVKKIIQDILCENSQVRHGHANLTFEQLRSLMESLFGKXVGAEDIEKTKACKP 302
QY 301 SDQILKLSLMRIKNGDQDTLKGLMHALKSHKTYHFKVTQSLKKTIRFLHSFTMYKLY 360
DB 303 SDQILKLSLMRIKNGDQDTLKGLMHALKSHKTYHFKVTQSLKKTIRFLHSFTMYKLY 362
QY 361 QKLFLEMIGNQVQSVKISCL 380
DB 363 QKLFLEMIGNQVQSVKISCL 382

RESULT 5
ADM28876

ID ADM28876 standard; protein; 385 AA.

XX
AC ADM28876;
XX

DT 20-MAY-2004 (first entry)

XX Human OPG truncation mutant, OPG met-met-(lys)3[22-401].
XX

Human; OPG; bone resorption; excessive bone loss; osteoporosis;
Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
Riley-day syndrome; immobilisation of extremity; tumour;
haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
renal function disorder; osteopaenia; osteonecrosis; bone cell death;
osteoprotegerin; transgenic; mutant; mutein.

XX Homo sapiens.
OS Synthetic.
XX US2003207827-A1.
XX 06-NOV-2003.
XX
XX 24-SEP-1999; 99US-00405032.
XX
XX 22-DEC-1995; 95US-00577788.
XX 03-SEP-1996; 96US-00706945.
XX 20-DEC-1996; 96US-00771777.
XX 12-AUG-1998; 98US-00132985.
XX
XX (BOYLE/) BOYLE W J.
XX (LACE/) LACEY D L.
XX (CALZ/) CALZONE F J.
XX (CHAN/) CHANG M.
XX
XX Boyle WJ, Lacey DL, Calzone FJ, Chang M;
XX WPI; 2004-041572/04.
XX
XX Novel osteoprotegerin useful for treating conditions resulting in bone
XX loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
XX loss caused by rheumatoid arthritis or osteomyelitis.
XX
XX Claim 37; Page; 141pp; English.
XX
XX The invention relates to a purified and isolated polypeptide having
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XX from carboxy terminus of human OPG polypeptide. Also included are an
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XX vector comprising OPG NA, a host cell transformed or transfected with the
XX vector, a transgenic mammal comprising the cell, producing OPG, a
XX polypeptide comprising an amino acid sequence of at least about 164 amino
XX acids comprising four cysteine-rich domains characteristic of the
XX cysteine rich domains of tumour necrosis factor receptor extracellular
XX regions (and an activity of increasing bone density), an antibody (Ab) or
XX its fragment which specifically binds to OPG, a composition comprising
XX OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
XX and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
XX Ab is useful for detecting the presence of OPG in a biological sample.
XX binding of Ab to OPG and detecting the bound Ab. OPG is useful for
XX assessing the ability of a candidate substance to bind to OPG. OPG NA is
XX useful for regulating the levels of OPG in an animal (human). The nucleic
XX acid promotes an increasing in tissue level of OPG. OPG is useful for
XX treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
XX disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
XX osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
XX osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
XX method further involves administering a substance chosen from bone
XX morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
XX inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
XX parathyroid hormone related protein and their analogues, E series of
XX prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
XX useful for treating osteoporosis such as primary osteoporosis, endocrine
XX osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
XX hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
XX, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
XX osteoporosis due to immobilisation of extremities, hypercalcaemia
XX resulting from solid tumours and haematologic malignancies (multiple
XX myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
XX hypercalcaemia associated with hyperthyroidism and renal function
XX disorders, osteopaenia following surgery and osteonecrosis or bone cell
XX death. The present sequences is an OPG truncation/deletion or
XX substitution mutant protein (or fragment).

Sequence 385 AA;

Query Match 100.0%; Score 2085; DB 8; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.2e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFPKYLHYDETSHTQLLCDKCPGTYLKQHTAKWKVVCAPCPDHYTDSHTSDECL 60
DB 6 ETFPKYLHYDETSHTQLLCDKCPGTYLKQHTAKWKVVCAPCPDHYTDSHTSDECL 65
QY 61 YCSPVCKELQYKQECNRTHNRVCECKGRYLEIFCLKHRSCPPGFGVVQAGTPPERNTV 120
DB 66 YCSPVCKELQYKQECNRTHNRVCECKGRYLEIFCLKHRSCPPGFGVVQAGTPPERNTV 125
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTKCGIDVTL 180
DB 126 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI CSGNSESTKCGIDVTL 185
QY 181 CBEAFPRFAVPKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSSEOETFQLLKWKHQN 240
DB 186 CBEAFPRFAVPKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSSEOETFQLLKWKHQN 245
QY 241 KAQDIVKKIIQDIDLCE NSVQRHIGHANLTFFQRLSRIMESLPCKKYGAEDIEKTIKACP 300
DB 246 KAQDIVKKIIQDIDLCE NSVQRHIGHANLTFFQRLSRIMESLPCKKYGAEDIEKTIKACP 305
QY 301 SDQILKLLSLWRINKGDDQTLKGLMEHALKHSKTYHFPKVTQSLKKTIRFLHSFTMYKLY 360
DB 306 SDQILKLLSLWRINKGDDQTLKGLMEHALKHSKTYHFPKVTQSLKKTIRFLHSFTMYKLY 365
QY 361 QKLFLFMIGNQVQSVKISCL 380
DB 366 QKLFLFMIGNQVQSVKISCL 385
RESULT 6
ADM28877
ID ADM28877 standard; protein; 391 AA.
XX
XX ADM28877;
XX
XX 20-MAY-2004 (first entry)
XX Human OPG truncation mutant, OPG met-met-arg-gly-ser- (His) 6 [22-401].
XX Human; OPG; bone resorption; excessive bone loss; osteoporosis;
XX Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
XX steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
XX osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
XX acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
XX Riley-day syndrome; immobilisation of extremity; tumour;
XX haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
XX renal function disorder; osteopaenia; osteonecrosis; bone cell death;
XX osteoprotegerin; transgenic; mutant; mutein.
XX
XX Homo sapiens.
XX Synthetic.
XX US2003207827-A1.
XX
XX 06-NOV-2003.
XX
XX 24-SEP-1999; 99US-00405032.
XX
XX 22-DEC-1995; 95US-00577788.
XX 03-SEP-1996; 96US-00706945.
XX 20-DEC-1996; 96US-00771777.
XX 12-AUG-1998; 98US-00132985.
XX
XX (BOYLE/) BOYLE W J.
XX (LACE/) LACEY D L.
XX (CALZ/) CALZONE F J.
XX (CHAN/) CHANG M.
XX
XX Boyle WJ, Lacey DL, Calzone FJ, Chang M;


```

XX      Sequence 400 AA;
SQ
Query Match      100.0%; Score 2085; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ETTPPKYLVHDEETSHQLLDCDCPPGTYLKQHCTAKWTVCACPDHYIYDTSWHTSDECL 60
DB      21  ETTPPKYLVHDEETSHQLLDCDCPPGTYLKQHCTAKWTVCACPDHYIYDTSWHTSDECL 80

QY      61  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVGVAQTPPENTV 120
DB      81  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVGVAQTPPENTV 140

QY      121  CKRCPDGFFSNETSAPCKRHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
DB      141  CKRCPDGFFSNETSAPCKRHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 200

QY      181  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKROHSSOBOTFQLLKLWKHQN 240
DB      201  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKROHSSOBOTFQLLKLWKHQN 260

QY      241  KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSIMESLPQKKGVAEDIEKTIKACP 300
DB      261  KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSIMESLPQKKGVAEDIEKTIKACP 320

QY      301  SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB      321  SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 380

QY      361  QKLFLEMIGNQVQSVKISCL 380
DB      381  QKLFLEMIGNQVQSVKISCL 400

RESULT 8
AAW38345
ID      AAW38345 standard; protein; 401 AA.
XX
AC      AAW38345;
XX
DT      20-APR-1998 (first entry)
XX
DE      Human osteoprotegerin.
XX
KW      Osteoprotegerin; antibody; diagnosis; affinity purification;
KW      recombinant production; transgenic animal; treatment; prevention;
KW      antisense oligonucleotide; probe; detection; screening; human;
KW      bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW      hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW      osteolytic metastasis; periodontal bone loss; bone necrosis; osteopaenia.
XX
OS      Homo sapiens.
XX
PN      D819654610-A1.
XX
PD      26-JUN-1997.
XX
PF      20-DEC-1996; 96DE-01054610.
XX
PR      22-DEC-1995; 95US-00577788.
PR      03-SEP-1996; 96US-00706945.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Boyle WJ, Lacey DL, Calzone FJ, Chang M;
XX
DR      WPI; 1997-334271/31.
XX
DR      N-PSDB; AAT96063.
XX
PT      Nucleic acid encoding osteoprotegerin - useful for treatment of diseases
PT      involving excessive bone loss, e.g. osteoporosis.

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XX      Claim 23; Page 109-111; 182pp; German.
XX
CC      The present sequence is human osteoprotegerin (OPG). Anti-OPG antibodies
CC      can be used in OPG diagnostic assays, and as affinity purification
CC      materials. The OPG cDNA can be used to express recombinant OPG and to
CC      generate transgenic animals. It can also be used to regulate the level of
CC      OPG in mammals, specifically to increase OPG levels, however the use of
CC      antisense sequences is also contemplated. Fragments of the cDNA can be
CC      used as probes to detect OPG expressing cells and tissue, and to screen
CC      cDNA libraries for related sequences. OPG can be used to treat or prevent
CC      bone diseases, specifically excessive bone loss, e.g. osteoporosis,
CC      Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
CC      arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
CC      bone necrosis and osteopaenia
XX
SQ      Sequence 401 AA;
Query Match      100.0%; Score 2085; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ETTPPKYLVHDEETSHQLLDCDCPPGTYLKQHCTAKWTVCACPDHYIYDTSWHTSDECL 60
DB      22  ETTPPKYLVHDEETSHQLLDCDCPPGTYLKQHCTAKWTVCACPDHYIYDTSWHTSDECL 81

QY      61  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVGVAQTPPENTV 120
DB      82  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVGVAQTPPENTV 141

QY      121  CKRCPDGFFSNETSAPCKRHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
DB      142  CKRCPDGFFSNETSAPCKRHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 201

QY      181  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKROHSSOBOTFQLLKLWKHQN 240
DB      202  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKROHSSOBOTFQLLKLWKHQN 261

QY      241  KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSIMESLPQKKGVAEDIEKTIKACP 300
DB      262  KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSIMESLPQKKGVAEDIEKTIKACP 321

QY      301  SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB      322  SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY      361  QKLFLEMIGNQVQSVKISCL 380
DB      382  QKLFLEMIGNQVQSVKISCL 401

RESULT 9
AAW43400
ID      AAW43400 standard; protein; 401 AA.
XX
AC      AAW43400;
XX
DT      28-JAN-2000 (first entry)
XX
DE      Osteoprotegerin protein sequence.
XX
KW      Osteoprotegerin; OPG; human; cardiovascular disease; occlusion;
KW      calcification; blood vessel; atherosclerosis; medial calcific sclerosis;
KW      Monckeberg's arteriosclerosis; therapy.
XX
OS      Homo sapiens.
XX
PN      WO9953942-A1.
XX
PD      28-OCT-1999.
XX
PF      21-APR-1999; 99WO-US008793.
XX

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PR 23-APR-1998; 98US-00064832.
XX (AMGE-) AMGEN INC.
XX Simonet S, Sarosi I;
XX WPI; 2000-013182/01.
DR N-PSDB; AAZ37254.
XX
PT Treating and preventing cardiovascular diseases, especially
PT atherosclerosis and Monckeberg's arteriosclerosis.
XX
PS Claim 9; Page 37-39; 43pp; English.
XX
CC This sequence represents the human osteoprotegerin (OPG). The invention
CC relates to a method of treating or preventing cardiovascular disease by
CC administering OPG. The method can be used to treat and prevent
CC cardiovascular diseases associated with occlusion and calcification of
CC blood vessels, especially atherosclerosis or Monckeberg's
CC arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or
CC prevent cardiovascular diseases provides an alternative to invasive
CC treatments. OPG can be used as a single therapeutic for prevention and
CC treatment of both osteoporosis and cardiovascular diseases
XX
SQ Sequence 401 AA;
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETPPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 60
DB 22 ETPPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 81
QY 61 YCSPVCKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNTV 120
DB 82 YCSPVCKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNTV 141
QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 180
DB 142 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNASVERIKRQHSQOEOTFOLLKWKHQN 240
DB 262 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLP GKKGVAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRKINGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRKINGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 OKLFLEMIGNQVSKISCL 380
DB 382 OKLFLEMIGNQVSKISCL 401
RESULT 10
ID AAB66976 standard; protein; 401 AA.
XX
AC AAB66976;
XX
DT 19-APR-2001 (first entry)
XX
DE Human OPG.
XX
KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
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KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
KW ischaemia; Parkinson's disease.
XX
OS Homo sapiens.
XX WO200103719-A2.
XX 18-JAN-2001.
XX
PF 07-JUL-2000; 2000WO-US018667.
XX
XX 09-JUL-1999; 99US-00350670.
XX 09-DEC-1999; 99US-00457647.
XX (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
WPI; 2001-103031/11.
DR N-PSDB; AAF57838.
XX
PT Treating conditions leading to bone loss such as rheumatoid arthritis,
PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
PT protein in conjunction with e.g. inhibitors of interleukin and tumor
PT necrosis factor alpha.
XX
PS Example 5; Fig 9; 316pp; English.
XX
CC The present invention relates to a method for treating conditions leading
CC to bone loss. The method comprises administering a purified and isolated
CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
CC in conjunction with other substances such as tumour necrosis factor-alpha
CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
CC modulators, fibroblast growth factor (FGF) 1-10 modulators and/or platelet
CC activating factor (PAF) antagonists. The method is useful for treating
CC conditions leading to bone loss such as rheumatoid arthritis, multiple
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
CC graft-versus-host disease (GVHD). Other diseases that can be treated
CC include acute pancreatitis, Alzheimer's disease, anorexia,
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
CC psoriasis and septic shock
XX
SQ Sequence 401 AA;
Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETPPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 60
DB 22 ETPPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 81
QY 61 YCSPVCKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNTV 120
DB 82 YCSPVCKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPGFGVQAGTPERNTV 141
QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 180
DB 142 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNASVERIKRQHSQOEOTFOLLKWKHQN 240
DB 262 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNASVERIKRQHSQOEOTFOLLKWKHQN 261
QY 241 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLP GKKGVAEDIEKTIKACKP 300
DB 262 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLP GKKGVAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRKINGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRKINGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 OKLFLEMIGNQVSKISCL 380
DB 382 OKLFLEMIGNQVSKISCL 401
```


Db 322 SDQILKLLSLWRIKNGDQTLKGLMHALKHSKTYHFKTVTQSLKKTIRFLHSFTMYKLY 381
 QY 361 QKLFLEMIGNOVQSVKISCL 380
 Db 382 QKLFLEMIGNOVQSVKISCL 401

RESULT 11
 ABG71823
 ID ABG71823 standard; protein; 401 AA.
 AC ABG71823;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Wild type human OPG (osteoprotegerin) protein.
 XX
 KW RANKL; human receptor activator of NFkappaB; osteoprotegerin; OPG;
 KW RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;
 KW osteoporosis; bone disease; human.
 XX
 OS Homo sapiens.
 XX
 PN W0200264782-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 08-FEB-2002; 2002WO-DK000090.
 XX
 PR 09-FEB-2001; 2001DK-00000214.
 PR 09-FEB-2001; 2001US-0267843P.
 PR 23-MAR-2001; 2001DK-00000498.
 PR 23-MAR-2001; 2001US-0278320P.
 XX
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX
 PI Haaning JM, Halkier T;
 XX
 DR WPI; 2002-691592/74.
 XX
 PT Novel human receptor activator of NFkappaB (hRANK) or human
 PT osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand
 PT (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for
 PT treating osteoporosis.
 XX
 PS Example 6; Fig 2; 129pp; English.
 XX
 CC This invention relates to a novel mutant proteins having an amino acid
 CC sequence that is different from and is at least about 70% identical to
 CC the amino acid sequence of human receptor activator of NFkappaB (hRANK)
 CC or human osteoprotegerin (hOPG), and which has a binding affinity to RANK
 CC ligand (RANKL) that is at least as high as the binding affinity of hRANK
 CC or hOPG to RANKL, as determined by functional competition assay. The
 CC protein of the invention may have osteopathic activity and may act as a
 CC RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity
 CC inhibitor. The nucleotide sequence shown in the invention may be used in
 CC gene therapy. The protein of the invention or fusion proteins comprising
 CC this protein are useful as a pharmaceutical, and in the preparation of a
 CC medicament for treating or preventing osteoporosis, or other bone
 CC diseases or diseases associated with binding of RANKL to the RANK
 CC receptor. A host cell containing a vector expressing the protein is
 CC useful for producing a polypeptide having binding affinity to RANKL,
 CC where the polypeptide comprises at least one N- or O-glycosylation site
 CC and the host cell is a eukaryotic host cell capable of in vivo
 CC glycosylation, and/or the polypeptide is subjected to conjugation to a
 CC non-polypeptide moiety in vitro. The protein of the invention has
 CC increased functional in vivo half-life and/or serum half-life compared to
 CC hRANK or hOPG and has an improved binding affinity to RANKL compared to
 CC the binding affinity of hRANK or hOPG to RANKL, as determined by a
 CC functional competition assay. The present sequence represents the human
 CC wild type OPG (osteoprotegerin) protein used to generate the mutant
 CC proteins invention

XX Sequence 401 AA;
 SQ
 Query Match 100.0%; Score 2085; DB 5; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.5e-153;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETEPPKYLHYDEETSHOILCDKCPGTYLKHCTAKWTKVACPCPDHYTDSWHTSDECL 60
 Db 22 ETEPPKYLHYDEETSHOILCDKCPGTYLKHCTAKWTKVACPCPDHYTDSWHTSDECL 81
 QY 61 YCSPVCKELQVVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERTV 120
 Db 82 YCSPVCKELQVVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERTV 141
 QY 121 CKRCPDFFSNETSAPCRKHTNCSVFGILLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
 Db 142 CKRCPDFFSNETSAPCRKHTNCSVFGILLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
 QY 181 CEEAFFRFAVPTKFTPNWLSVLDNLPFGTKVNAESVERIKRQHSOFTQLLKLWKHQN 240
 Db 202 CEEAFFRFAVPTKFTPNWLSVLDNLPFGTKVNAESVERIKRQHSOFTQLLKLWKHQN 261
 QY 241 KAQDIVKKIIQDIDL CENSQRHIGHANLTFEQLRSIMESLPKKGVAEDIEKTIKACKP 300
 Db 262 KAQDIVKKIIQDIDL CENSQRHIGHANLTFEQLRSIMESLPKKGVAEDIEKTIKACKP 321
 QY 301 SDQILKLLSLWRIKNGDQTLKGLMHALKHSKTYHFKTVTQSLKKTIRFLHSFTMYKLY 360
 Db 322 SDQILKLLSLWRIKNGDQTLKGLMHALKHSKTYHFKTVTQSLKKTIRFLHSFTMYKLY 381
 QY 361 QKLFLEMIGNOVQSVKISCL 380
 Db 382 QKLFLEMIGNOVQSVKISCL 401

RESULT 12
 ABP55109
 ID ABP55109 standard; protein; 401 AA.
 XX
 AC ABP55109;
 XX
 DT 05-FEB-2003 (first entry)
 XX
 DE Human osteoprotegerin receptor.
 XX
 KW Osteoprotegerin; receptor; OPG; human; autoimmune disease;
 KW rheumatoid arthritis; diabetes; osteoarthritis; psoriasis;
 KW inflammatory bowel disease; transplant rejection; allergy;
 KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
 KW antipsoriatic; immunosuppressive; antiallergic; antiinflammatory;
 KW osteopathic; antitumor; monocytic.
 XX
 OS Homo sapiens.
 XX
 PN W0200276507-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 06-FEB-2002; 2002WO-US001238.
 XX
 PR 23-MAR-2001; 2001US-0278215P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Grewal I;
 XX
 DR WPI; 2003-058352/05.
 DR N-PSDB; ABV75843.
 XX
 PT Stimulating mammalian monocytes by exposing to an OPG ligand polypeptide,
 PT useful for treating immune related disorders such as autoimmune disease,
 PT rheumatoid arthritis, diabetes, osteoarthritis, psoriasis, and allergy.

XX Disclosure; Fig 2B; 11lpp; English.

PS The present sequence is the protein sequence of human osteoprotegerin

XX (OPG) receptor. The invention provides methods of using OPG ligand (OPGL)

CC to activate monocytes to secrete chemokines or cytokines by exposing a

CC mammalian cell (in cell culture or in a mammal) to OPGL. Also provided

CC are methods of using OPGL to treat conditions or diseases in mammals

CC associated with, or resulting from lack of, or decreased, chemokine or

CC cytokine secretion by monocytes. The invention also provides OPG agonist

CC and antagonist molecules to modulate immune activity. These may include

CC antibodies to the OPG or RANK receptors. An antagonist comprising an anti

CC -OPGL antibody, an anti-OPG receptor antibody, an anti-RANK receptor

CC antibody, an OPG receptor immunoadhesin or a RANK receptor immunoadhesin

CC is used in a claimed method of treating an immune-related condition,

CC especially an autoimmune disease, rheumatoid arthritis, insulin dependent

CC diabetes, osteoarthritis, inflammatory bowel disease (especially

CC ulcerative colitis or Crohn's disease), psoriasis, transplant rejection

CC or allergy

XX Sequence 401 AA;

SQ

Query Match 100.0%; Score 2085; DB 6; Length 401;

Best Local Similarity 100.0%; Pred. No. 5.5e-153;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFFPKYLHYDETSKQPCGTYLKHQCTAKWTVACPDHYVYDTSWHTSDECL 60

DB 22 ETFFPKYLHYDETSKQPCGTYLKHQCTAKWTVACPDHYVYDTSWHTSDECL 81

QY 61 YGSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKXRSPPGFGVQAGTPERNTV 120

DB 82 YGSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKXRSPPGFGVQAGTPERNTV 141

QY 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTOKCGIDVTL 180

DB 142 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTOKCGIDVTL 201

QY 181 CSEAFRRFPAVPTKFTPNWLSVLVDNLPKTVNAESVERIKRQHSQEQTFQLLKLWKHQN 240

DB 202 CSEAFRRFPAVPTKFTPNWLSVLVDNLPKTVNAESVERIKRQHSQEQTFQLLKLWKHQN 261

QY 241 KQADIVKKIIQDIDLCEMSVQRHGHANITFEQLRSLMESLPKVKVGAEDIEKTIKACP 300

DB 262 KQADIVKKIIQDIDLCEMSVQRHGHANITFEQLRSLMESLPKVKVGAEDIEKTIKACP 321

QY 301 SQDILKLLSLWRIKNGDQDTLKLMLHAKSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 360

DB 322 SQDILKLLSLWRIKNGDQDTLKLMLHAKSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLEMIGNQVQSVKISCL 380

DB 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 13

AAE34363

ID AAE34363 standard; protein; 401 AA.

XX AAE34363;

AC AAE34363;

XX

14-MAY-2003 (first entry)

DE Human osteoprotegerin (OPG) protein.

XX

KW Human; acute septic arthritis; osteomalacia; hyperparathyroidism;

KW Cushing's syndrome; receptor activator of NF-kappa B; cancer; scurvy;

KW bone formation; rickets; Langerhan's cell histiocytosis; gene therapy;

KW monocrotic fibrous dysplasia; radiation therapy; spinal cord injury;

KW RANK; Gaucher's disease; polyostotic fibrous dysplasia; OPG;

KW osteoprotegerin.

XX

OS Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..21

FT Protein 22..401

XX /label= Signal_peptide

XX /note= "Mature OPG protein"

PN WO200292016-A2.

XX 21-NOV-2002.

XX 17-MAY-2002; 2002WO-US016002.

XX 17-MAY-2001; 2001US-0291919P.

XX (IMNV) IMMUNEX CORP.

XX Dougall WC, Anderson DM;

XX WPI; 2003-129220/12.

XX N-PSDB; AAD52597.

XX Treating patients having e.g. acute septic arthritis, osteomalacia,

XX hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises

XX administering a receptor activator of NF-kappa B antagonist to increase

XX bone formation.

XX Claim 1; Page 47-49; 52pp; English.

XX The invention relates to a method of treating a patient having e.g. acute

XX septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome

XX or spinal cord injury. The method involves administering a receptor

XX activator of NF-kappa B (RANK) antagonist to stimulate an increase in the

XX rate for formation of new bone. RANK antagonist is capable of inhibiting

XX the ability of RANK to induce NF-kappa B. The method is useful for

XX stimulating bone formation, or for treating patients having acute septic

XX arthritis, osteomalacia (including rickets and scurvy),

XX hyperparathyroidism, Cushing's syndrome, monocrotic fibrous dysplasia,

XX polyostotic fibrous dysplasia, Gaucher's disease, Langerhan's cell

XX histiocytosis, spinal cord injury, patients requiring periodontal

XX reconstruction, or patients who have completed a course or radiation

XX therapy for cancer. The method is also useful for treating a patient who

XX is a prosthetic joint recipient, a bone graft recipient, or a ligament

XX graft recipient. The invention is useful in gene therapy. The present

XX sequence is human osteoprotegerin (OPG). OPG serves as human RANK

XX antagonist

XX Sequence 401 AA;

SQ

Query Match 100.0%; Score 2085; DB 6; Length 401;

Best Local Similarity 100.0%; Pred. No. 5.5e-153;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFFPKYLHYDETSKQPCGTYLKHQCTAKWTVACPDHYVYDTSWHTSDECL 60

DB 22 ETFFPKYLHYDETSKQPCGTYLKHQCTAKWTVACPDHYVYDTSWHTSDECL 81

QY 61 YGSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKXRSPPGFGVQAGTPERNTV 120

DB 82 YGSPVCKELQYVQECNTHNRVCECKEGRYLEIEFCLKXRSPPGFGVQAGTPERNTV 141

QY 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTOKCGIDVTL 180

DB 142 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSENSTOKCGIDVTL 201

QY 181 CSEAFRRFPAVPTKFTPNWLSVLVDNLPKTVNAESVERIKRQHSQEQTFQLLKLWKHQN 240

DB 202 CSEAFRRFPAVPTKFTPNWLSVLVDNLPKTVNAESVERIKRQHSQEQTFQLLKLWKHQN 261

QY 241 KQADIVKKIIQDIDLCEMSVQRHGHANITFEQLRSLMESLPKVKVGAEDIEKTIKACP 300

DB 262 KQADIVKKIIQDIDLCEMSVQRHGHANITFEQLRSLMESLPKVKVGAEDIEKTIKACP 321

QY 301 SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKVTQSLKKTIRFLHSFTMYKLY 360
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 Db 322 SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKVTQSLKKTIRFLHSFTMYKLY 381
 |||
 QY 361 QKLFLFLEMIGNQVQSVKISCL 380
 |||
 Db 382 QKLFLFLEMIGNQVQSVKISCL 401
 |||

RESULT 14
 ADD01627
 ID ADD01627 standard; protein; 401 AA.
 XX
 AC ADD01627;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human osteoprotegerin amino acid sequence SEQ ID NO:4.
 XX
 KW fibrotic disease; cysteine-rich domain; osteoprotegerin; scleroderma;
 KW antiinflammatory; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003084560-A2.
 XX
 PD 16-OCT-2003.
 XX
 XX 26-MAR-2003; 2003WO-EP050080.
 PF
 XX 10-APR-2002; 2002EP-00100364.
 PR
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 PA
 XX Power C, Plater-Zyberk C;
 PI
 XX WPI; 2003-804248/75.
 DR
 DR N-PSDB; ADD01626.
 XX
 XX Use of a substance for the manufacture of a medicament for treating or
 PT preventing fibrotic disease.
 PT
 XX Claim 1; SEQ ID NO 4; 68pp; English.
 PS
 CC The present invention describes a substance which is useful for the
 CC manufacture of a medicament for treating or preventing fibrotic disease.
 CC The substance comprises: (a) a polypeptide comprising a fully defined
 CC sequence having 401 amino acids (see ADD01625 and ADD01627), or its amino
 CC acids 22-401 or 22-194; (b) a polypeptide comprising 1, 2, 3 or 4
 CC cysteine-rich domains of osteoprotegerin; (c) a mutin of (a)-(b) that is
 CC encoded by a DNA sequence that hybridises to the complement of the DNA
 CC sequence encoding (a)-(b) under moderately or highly stringent conditions
 CC ; where the amino acid sequence has at least 40, 50, 60, 70, 80 or 90%
 CC identity with (a)-(b); and where any changes in the amino acid sequence
 CC are conservative amino acid substitutions to the amino acid sequences in
 CC (a)-(b); or (d) a salt or an isoform, fused protein, functional
 CC derivative, active fraction or circularly permuted derivative of (a)-
 CC (c). Also described: (1) a polypeptide comprising the 401-amino acid
 CC sequence and one, two, three or four cysteine-rich domains of
 CC osteoprotegerin; and (2) a method for treating or preventing a fibrotic
 CC disease, particularly scleroderma. The substance has antiinflammatory
 CC activity, and can be used in gene therapy. A vector or cell comprising
 CC the nucleic acid molecule encoding a polypeptide of the invention can be
 CC used for inducing or enhancing the endogenous production of the
 CC polypeptide in a cell for the preparation of a medicament for treating or
 CC preventing a fibrotic disease, in particular scleroderma. The present
 CC sequence represents a human osteoprotegerin amino acid sequence which is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 401 AA;

Query Match 100.0%; Score 2085; DB 7; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.5e-153;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFFPPKYLHYDETSHQLLCDKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 |||
 Db 22 ETFFPPKYLHYDETSHQLLCDKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
 |||
 QY 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVQAGTPERNTV 120
 |||
 Db 82 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVQAGTPERNTV 141
 |||
 QY 121 CKRCPDGFFSNETSSKAPCKHTNCSVFGLLLTQKGNATHDNTCSGNSESTQKGDVTL 180
 |||
 Db 142 CKRCPDGFFSNETSSKAPCKHTNCSVFGLLLTQKGNATHDNTCSGNSESTQKGDVTL 201
 |||
 QY 181 CEEAFFFAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQSSQEQIFQLKLWKHQN 240
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 Db 202 CEEAFFFAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQSSQEQIFQLKLWKHQN 261
 |||
 QY 241 KAQDIVKKIIQIDILCENSQVRHIGHANLTFEQLRSIMESLPCKYKGAEDIEKTIKACKP 300
 |||
 Db 262 KAQDIVKKIIQIDILCENSQVRHIGHANLTFEQLRSIMESLPCKYKGAEDIEKTIKACKP 321
 |||
 QY 301 SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKVTQSLKKTIRFLHSFTMYKLY 360
 |||
 Db 322 SDQILKLLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKVTQSLKKTIRFLHSFTMYKLY 381
 |||
 QY 361 QKLFLFLEMIGNQVQSVKISCL 380
 |||
 Db 382 QKLFLFLEMIGNQVQSVKISCL 401
 |||

RESULT 15
 ADM28813
 ID ADM28813 standard; protein; 401 AA.
 XX
 AC ADM28813;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human osteoprotegerin, OPG.
 XX
 KW Human; OPG; bone resorption; excessive bone loss; osteoporosis;
 KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
 KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
 KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
 KW Riley-day syndrome; immobilisation of extremity; tumour;
 KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
 KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
 KW osteoprotegerin; transgenic.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 Peptide 1..21
 Protein /note= "Signal peptide"
 FT 22..401 /note= "Mature OPG, claimed in claim 24"
 FT 22..201 /note= "Claimed in claim 32"
 FT 22..194 /note= "Claimed in claim 32"
 FT 22..189 /note= "Claimed in claim 32"
 FT 22..185 /note= "Claimed in claim 32"
 FT 27..401 /note= "Claimed in claim 35"
 FT 27..194 /note= "Claimed in claim 35"
 FT 27..189 /note= "Claimed in claim 35"
 FT 27..185 /note= "Claimed in claim 35"

FT /note= "Claimed in claim 35"
FT 32. .401
XX /note= "Claimed in claim 25"

PN US2003207827-A1.

XX 06-NOV-2003.

XX 24-SEP-1999; 99US-00405032.

XX 22-DEC-1995; 95US-00577788.

PR 03-SEP-1996; 96US-00706945.

PR 20-DEC-1996; 96US-00771777.

PR 12-AUG-1998; 98US-00132985.

XX (BOYL/) BOYLE W J.

PA (LACE/) LACEY D L.

PA (CALZ/) CALZONE F J.

PA (CHAN/) CHANG M.

PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX WPI; 2004-041572/04.

DR N-PSDB; ADM28812.

XX Novel osteoprotegerin useful for treating conditions resulting in bone

PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone

PT loss caused by rheumatoid arthritis or osteomyelitis.

XX Claim 23; SEQ ID NO 125; 141pp; English.

XX The invention relates to a purified and isolated polypeptide having
CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
CC having amino terminus at residue 22, and 1-216 amino acids are deleted
CC from carboxy terminus of human OPG polypeptide. Also included are an
CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
CC vector comprising OPG NA, a host cell transformed or transfected with the
CC polypeptide comprising an amino acid sequence of at least about 164 amino
CC acids comprising four cysteine-rich domains characteristic of the
CC cysteine rich domains of tumour necrosis factor receptor extracellular
CC regions (and an activity of increasing bone density), an antibody (Ab) or
CC its fragment which specifically binds to OPG, a composition comprising
CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
CC Ab is useful for detecting the presence of OPG in a biological sample
CC which involves incubating the sample with Ab under conditions that allow
CC binding of ab to OPG and detecting the bound Ab. OPG is useful for
CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
CC useful for regulating the levels of OPG in an animal (human). The nucleic
CC acid promotes an increasing in tissue level of OPG. OPG is useful for
CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
CC method further involves administering a substance chosen from bone
CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
CC parathyroid hormone related protein and their analogues, E series of
CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
CC useful for treating osteoporosis such as primary osteoporosis, endocrine
CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
CC osteoporosis due to immobilisation of extremities, hypercalcaemia
CC resulting from solid tumours and haematologic malignancies (multiple
CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
CC hypercalcaemia associated with hyperthyroidism and renal function
CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
CC death. The present sequences is an OPG protein (or fragment).

XX Sequence 401 AA;

Query Match		100.0%;	Score 2085;	DB 8;	Length 401;
Best Local Similarity		100.0%;	Pred. No. 5.5e-153;		
Matches 380;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	22	ETFPKYLHYDEETSHQLL	CDKCPPGTYLKHCTAKWTV	CAPCDPHYTTDSWHTSDECL	81
QY	61	YCSVPCKELQYVKQCN	RTHRVCECKGRYLEIEFCL	KHRSCEPGFGVVGAGTPERNTV	120
Db	82	YCSVPCKELQYVKQCN	RTHRVCECKGRYLEIEFCL	KHRSCEPGFGVVGAGTPERNTV	141
QY	121	CKRCPDGFSSNETSSK	APCRKHTNCSVFGLLTQK	GNATHDNICSGNSESTQKCGIDVTL	180
Db	142	CKRCPDGFSSNETSSK	APCRKHTNCSVFGLLTQK	GNATHDNICSGNSESTQKCGIDVTL	201
QY	181	CEAFFFFRAVPTKFT	PNWLSVLVDNLPGTKVNA	ESVERIKQHSQEQTFQLLKLWKHQN	240
Db	202	CEAFFFFRAVPTKFT	PNWLSVLVDNLPGTKVNA	ESVERIKQHSQEQTFQLLKLWKHQN	261
QY	241	KAQDIVKKIIQDIDL	CENSQVORHIGHANLT	FEQLRSLMESLPGKKVGAEDIEKTIKACP	300
Db	262	KAQDIVKKIIQDIDL	CENSQVORHIGHANLT	FEQLRSLMESLPGKKVGAEDIEKTIKACP	321
QY	301	SDQILKLLSLWRIK	NGDDDTLKGLMEALKH	SKTYHFPKTVTQSLKKTIRFLHSFTMYKLY	360
Db	322	SDQILKLLSLWRIK	NGDDDTLKGLMEALKH	SKTYHFPKTVTQSLKKTIRFLHSFTMYKLY	381
QY	361	QKLFLEMIGNOVQSV	KISCL	380	
Db	382	QKLFLEMIGNOVQSV	KISCL	401	

Search completed: November 15, 2004, 19:00:23

Job time : 164 secs

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OM protein - protein search, using sw model

Run on: November 15, 2004, 18:51:06 ; Search time 47 Seconds
(without alignments)
536.188 Million cell updates/sec

Title: US-10-676-358-1

Perfect score: 2085

Sequence: 1 ETFPKYLHYDETHSHQLLC.....QKLFLEMGVQSVKISCL 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2085	100.0	401	3	US-08-974-022-6
2	2085	100.0	401	3	US-09-042-785A-12
3	2085	100.0	401	3	US-08-795-445A-6
4	2085	100.0	401	3	US-08-795-447A-6
5	2085	100.0	401	3	US-08-974-186-6
6	2085	100.0	401	3	US-08-795-446B-6
7	2085	100.0	401	3	US-08-706-945D-128
8	2085	100.0	401	4	US-08-577-788C-6
9	2085	100.0	401	4	US-08-577-788C-56
10	2085	100.0	401	4	US-09-064-832-2
11	2079	99.7	401	3	US-09-153-927-1
12	2079	99.7	401	3	US-09-072-993C-1
13	1982	95.1	364	3	US-08-706-945D-142
14	1828	87.7	401	3	US-08-974-022-2
15	1828	87.7	401	3	US-08-795-445A-2
16	1828	87.7	401	3	US-08-795-447A-2
17	1828	87.7	401	3	US-08-974-186-2
18	1828	87.7	401	3	US-08-795-446B-2
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22	1820	87.3	401	3	US-08-974-022-4
23	1820	87.3	401	3	US-09-042-785A-13
24	1820	87.3	401	3	US-08-795-445A-4
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27	1820	87.3	401	3	US-08-795-446B-4

28	1820	87.3	401	3	US-08-706-945D-126
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31	1720	82.5	364	3	US-08-706-945D-141
32	1531	73.4	293	4	US-09-896-096A-18
33	952	45.7	208	4	US-08-577-788C-50
34	945	45.3	161	4	US-09-632-277A-3
35	865	41.5	147	3	US-09-527-236A-20
36	865	41.5	147	4	US-09-756-854-20
37	861	41.3	146	4	US-09-523-323-58
38	827	39.7	139	3	US-08-706-945D-130
39	781	37.5	174	3	US-08-706-945D-136
40	440.5	21.1	300	2	US-08-794-796-2
41	440.5	21.1	300	4	US-09-632-277A-2
42	440.5	21.1	300	4	US-09-523-323-52
43	440.5	21.1	300	4	US-09-896-096A-1
44	433	20.8	211	3	US-09-286-529-20
45	432	20.7	299	3	US-09-286-529-17

ALIGNMENTS

RESULT 1

US-08-974-022-6

; Sequence 6, Application US/08974022

; Patent No. 6015938

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

; APPLICANT: Calzone, Frank J.

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: OSTEOPROTEGERIN

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,022

; FILING DATE: 12-DEC-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/577,788

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-378

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 401 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-974-022-6

Query Match 100.0%; Score 2085; DB 3; Length 401;

Best Local Similarity 100.0%; Pred. No. 2.4e-186;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDETHSHQLLCDCPCPGTYLKQHCTAKWTVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFPKYLHYDETHSHQLLCDCPCPGTYLKQHCTAKWTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVCKELQYVKQECNRTNTHVCSCKEGRYLEIFCLKHSRCPFGFGVQAGTERTNV 120

Db 82 YCSFVKELQVQECNRTNRVCECKRGYLEIEFCLKHSRCPGFGVVOAGTPERNTV 141
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCVPGLLLTOKGNATHNICSGNSESTOKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCVPGLLLTOKGNATHNICSGNSESTOKCGIDVTL 201
Qy 181 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKWKHON 240
Db 202 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKWKHON 261
Qy 241 KAQDVIKKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 300
Db 262 KAQDVIKKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 321
Qy 301 SDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
Qy 361 OKLFLEMIGNOVQSVKISCL 380
Db 382 OKLFLEMIGNOVQSVKISCL 401

RESULT 2
US-09-042-785A-12
; Sequence 12, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSES: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-12

Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ETFFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
Qy 61 YCSFVKELQVQECNRTNRVCECKRGYLEIEFCLKHSRCPGFGVVOAGTPERNTV 120
Db 82 YCSFVKELQVQECNRTNRVCECKRGYLEIEFCLKHSRCPGFGVVOAGTPERNTV 141
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCVPGLLLTOKGNATHNICSGNSESTOKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCVPGLLLTOKGNATHNICSGNSESTOKCGIDVTL 201
Qy 181 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKWKHON 240
Db 202 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKWKHON 261
Qy 241 KAQDVIKKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 300
Db 262 KAQDVIKKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 321
Qy 301 SDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
Qy 361 OKLFLEMIGNOVQSVKISCL 380
Db 382 OKLFLEMIGNOVQSVKISCL 401

RESULT 3
US-08-795-445A-6
; Sequence 6, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-6

Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ETFFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFFPKYLHYDEETSHQLLCKDPCPGTYLKQCHTAKWKTVCAPCPDHYHYTDSWHTSDECL 81
YQ 61 YCSPVCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERTV 120
Db 82 YCSPVCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERTV 141
YQ 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
YQ 181 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSEQOTFOLLKLWKHQN 240
Db 202 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSEQOTFOLLKLWKHQN 261
YQ 241 KAODIVVKIQQIDILCENSQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAODIVVKIQQIDILCENSQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
YQ 301 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 381
YQ 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 4
US-08-795-447A-6
; Sequence 6, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-447A-6
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1 ETFFPKYLHYDEETSHQLLCKDPCPGTYLKQCHTAKWKTVCAPCPDHYHYTDSWHTSDECL 60
Db 22 ETFFPKYLHYDEETSHQLLCKDPCPGTYLKQCHTAKWKTVCAPCPDHYHYTDSWHTSDECL 81

YQ 61 YCSPVCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERTV 120
Db 82 YCSPVCKELQVVKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERTV 141
YQ 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
YQ 181 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSEQOTFOLLKLWKHQN 240
Db 202 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSEQOTFOLLKLWKHQN 261
YQ 241 KAODIVVKIQQIDILCENSQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAODIVVKIQQIDILCENSQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
YQ 301 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 381
YQ 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 5
US-08-974-186-6
; Sequence 6, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-186-6
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1 ETFFPKYLHYDEETSHQLLCKDPCPGTYLKQCHTAKWKTVCAPCPDHYHYTDSWHTSDECL 60
Db 22 ETFFPKYLHYDEETSHQLLCKDPCPGTYLKQCHTAKWKTVCAPCPDHYHYTDSWHTSDECL 81

Db 22 ETFPKYLHYDEETSHQLLCKPPTGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQVVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNIV 120
Db 82 YCSPVCKELQVVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEQTFOLLKLWKHQH 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEQTFOLLKLWKHQH 261
QY 241 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRINKNGDQDTL KGLMHALKHKSHTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRINKNGDQDTL KGLMHALKHKSHTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 6

US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-446B-6
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFPKYLHYDEETSHQLLCKPPTGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFPKYLHYDEETSHQLLCKPPTGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQVVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNIV 120
Db 82 YCSPVCKELQVVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEQTFOLLKLWKHQH 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEQTFOLLKLWKHQH 261
QY 241 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRINKNGDQDTL KGLMHALKHKSHTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRINKNGDQDTL KGLMHALKHKSHTYHFFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 7

US-08-706-945D-128
; Sequence 128, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 128
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-128
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFPKYLHYDEETSHQLLCKPPTGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLLCKPPTGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQVVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNIV 120
Db 82 YCSPVCKELQVVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEQTFOLLKLWKHQH 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEQTFOLLKLWKHQH 261
QY 241 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300

Db 262 KAQDIVKKIIQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 321
QY 301 SDQILKLSLWRINKGDDTLKGLMHALKSKTYHPKTVTQSLKKTIRFLHSFTWKLY 360
Db 322 SDQILKLSLWRINKGDDTLKGLMHALKSKTYHPKTVTQSLKKTIRFLHSFTWKLY 381
QY 361 QKLFLMIGNQVQSVKISCL 380
Db 382 QKLFLMIGNQVQSVKISCL 401

RESULT 8

US-08-577-788C-6
; Sequence 6, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-577-788C-6

Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 120
Db 82 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 141
QY 121 CKRCPDGFFSNETS SKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQKCGIDVTL 180
Db 142 CKRCPDGFFSNETS SKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQN 240
Db 202 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQN 261
QY 241 KAQDIVKKIIQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
Db 262 KAQDIVKKIIQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 321
QY 301 SDQILKLSLWRINKGDDTLKGLMHALKSKTYHPKTVTQSLKKTIRFLHSFTWKLY 360
Db 322 SDQILKLSLWRINKGDDTLKGLMHALKSKTYHPKTVTQSLKKTIRFLHSFTWKLY 381
QY 361 QKLFLMIGNQVQSVKISCL 380
Db 382 QKLFLMIGNQVQSVKISCL 401

RESULT 9

US-08-577-788C-56
; Sequence 56, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank

; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-577-788C-56

Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 120
Db 82 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 141
QY 121 CKRCPDGFFSNETS SKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQKCGIDVTL 180
Db 142 CKRCPDGFFSNETS SKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQN 240
Db 202 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQN 261
QY 241 KAQDIVKKIIQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
Db 262 KAQDIVKKIIQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 321
QY 301 SDQILKLSLWRINKGDDTLKGLMHALKSKTYHPKTVTQSLKKTIRFLHSFTWKLY 360
Db 322 SDQILKLSLWRINKGDDTLKGLMHALKSKTYHPKTVTQSLKKTIRFLHSFTWKLY 381
QY 361 QKLFLMIGNQVQSVKISCL 380
Db 382 QKLFLMIGNQVQSVKISCL 401

RESULT 10

US-09-064-832-2
; Sequence 2, Application US/09064832
; Patent No. 6730823
; GENERAL INFORMATION:
; APPLICANT: Simonet, Scott
; APPLICANT: Sarosi, Ildiko
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; PREVENTION AND TREATMENT OF CARDIOVASCULAR DISEASES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,832
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-064-832-2

Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 60
DB 22 ETFPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 81

QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCLPPGFGVQAGTPERNTV 120
DB 82 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCLPPGFGVQAGTPERNTV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201

QY 181 CEEAFFRAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOFTQLLKLWKHON 240
DB 202 CEEAFFRAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOFTQLLKLWKHON 261

QY 241 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
DB 262 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 321

QY 301 SDQILKLLSLWRIKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRIKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 382 QKLFLEMIGNOVQSVKISCL 401

RESULT 11
US-09-153-927-1
; Sequence 1, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-1

Query Match 99.7%; Score 2079; DB 3; Length 401;
Best Local Similarity 99.7%; Pred. No. 8.5e-186;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 60
DB 22 ETFPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 81

DB 22 ETFPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 81
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCLPPGFGVQAGTPERNTV 120
DB 82 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCLPPGFGVQAGTPERNTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOFTQLLKLWKHON 240
DB 202 CEEAFFRAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOFTQLLKLWKHON 261
QY 241 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
DB 262 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRIKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRIKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 382 QKLFLEMIGNOVQSVKISCL 401

RESULT 12
US-09-072-993C-1
; Sequence 1, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-1

Query Match 99.7%; Score 2079; DB 3; Length 401;
Best Local Similarity 99.7%; Pred. No. 8.5e-186;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 60
DB 22 ETFPKYLHYDEETSHQLLCKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDCL 81
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCLPPGFGVQAGTPERNTV 120
DB 82 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCLPPGFGVQAGTPERNTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOFTQLLKLWKHON 240
DB 202 CEEAFFRAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOFTQLLKLWKHON 261

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QY 241 KAQDIVKKIIQIDILCENSQVORHIGHANLTFEOLRSIMESLPKKVGAEDEIKTIKACP 300
Db 262 KQDIVKKIIQIDILCENSQVORHIGHANLTFEOLRSIMESLPKKVGAEDEIKTIKACP 321
QY 301 SDQILKLLSWRIKNGDQDILKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSWRIKNGDQDILKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLFLEMIGNQVQSVKISCL 401

RESULT 13
US-08-706-945D-142
; Sequence 142, Application US/08706945D
; Patent No. 8369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-706-945D-142
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Query Match 95.1%; Score 1982; DB 3; Length 364;
Best Local Similarity 95.8%; Pred. No. 8.6e-177;
Matches 364; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

QY 1 ETEPPKYLHYDEETSHQLLDCPCPPGTLYLKQHCTAKWKTVCACPDHYHYTDSWHTSDECL 60
Db 1 ETEPPKYLHYDEETSHQLLDCPCPPGTLYLKQHCTAKWKTVCACPDHYHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVQECNRTNRNVCCEKGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 120
Db 61 YCSPVKELQYVQECNRTNRNVCCEKGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 120
QY 121 CKRCPDGFFSNETSAPCRKHTNCSVFGILLTQKGNATHDNCNCSGSESTQKCGIDVTLL 180
Db 121 CKRCPDGFFSNETSAPCRKHTN-----DNICSGNSESTQKCGIDVTLL 164
QY 181 CEEAFFRFAVPTFTFNWLSVLVDNLPGTKVNAESVERIKROHSSQEQTFQLLKLWKHQN 240
Db 165 CEEAFFRFAVPTFTFNWLSVLVDNLPGTKVNAESVERIKROHSSQEQTFQLLKLWKHQN 224
QY 241 KAQDIVKKIIQIDILCENSQVORHIGHANLTFEOLRSIMESLPKKVGAEDEIKTIKACP 300
Db 225 KAQDIVKKIIQIDILCENSQVORHIGHANLTFEOLRSIMESLPKKVGAEDEIKTIKACP 284
QY 301 SDQILKLLSWRIKNGDQDILKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 285 SDQILKLLSWRIKNGDQDILKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 344
QY 361 QKLFLFLEMIGNQVQSVKISCL 380
Db 345 QKLFLFLEMIGNQVQSVKISCL 364
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RESULT 14
US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
```

```
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-2

Query Match 87.7%; Score 1828; DB 3; Length 401;
Best Local Similarity 86.3%; Pred. No. 2.4e-162;
Matches 328; Conservative 24; Mismatches 28; Indels 0; Gaps 0;

QY 1 ETEPPKYLHYDEETSHQLLDCPCPPGTLYLKQHCTAKWKTVCACPDHYHYTDSWHTSDECL 60
Db 22 ETEPPKYLHYDPTGQQLLDCPCAPGTLYLKQHCTVRKTLVCPDYSYTDWHTSDECL 81
QY 61 YCSPVKELQYVQECNRTNRNVCCEKGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 120
Db 82 YCSPVKELQYVQECNRTNRNVCCEKGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 141
QY 121 CKRCPDGFFSNETSAPCRKHTNCSVFGILLTQKGNATHDNCNCSGSESTQKCGIDVTLL 180
Db 142 CKRCPDGFFSGETSSAPCRKHTNCSLGLLLTQKGNATHDNCNCSGSESTQKCGIDVTLL 201
QY 181 CEEAFFRFAVPTFTFNWLSVLVDNLPGTKVNAESVERIKROHSSQEQTFQLLKLWKHQN 240
Db 202 CEEAFFRFAVPTKIIINWLSVLVDLPGTKVNAESVERIKRHSQEQTFQLLKLWKHQN 261
QY 241 KAQDIVKKIIQIDILCENSQVORHIGHANLTFEOLRSIMESLPKKVGAEDEIKTIKACP 300
Db 262 RDQEMVKKIIQIDILCESSQVORHIGHANLTFEOLRILMESLPKKISPOEIERTRKTCXP 321
QY 301 SDQILKLLSWRIKNGDQDILKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SEOLLKLLSWRIKNGDQDILKGLMYALKHLKAYHFPKTVTTHSLRKTIRFLHSFTMYRLY 381
QY 361 QKLFLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLFLEMIGNQVQSVKISCL 401

RESULT 15
US-08-795-445A-2
; Sequence 2, Application US/08795445A
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Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	2085	100.0	380	10	US-09-405-032-139	Sequence
2	2085	100.0	380	16	US-10-676-358-1	Sequence
3	2085	100.0	400	14	US-10-142-658-2	Sequence
4	2085	100.0	401	10	US-09-405-032-125	Sequence
5	2085	100.0	401	14	US-10-151-071-8	Sequence
6	2085	100.0	401	16	US-10-467-243-2	Sequence
7	2085	100.0	537	16	US-10-676-358-6	Sequence
8	2079	99.7	380	9	US-09-062-113-4	Sequence 4
9	2079	99.7	380	14	US-10-233-858-4	Sequence 4
10	2079	99.7	380	16	US-10-785-109-4	Sequence 4
11	2079	99.7	380	16	US-10-785-114-4	Sequence 4
12	2079	99.7	391	9	US-09-062-113-106	Sequence 1
13	2079	99.7	391	14	US-10-233-858-106	Sequence 1

Query Match 100.0%; Score 2085; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.9e-167; Indels 0; Gaps 0;
Matches 380; Conservative 0; Mismatches 0;

QY 1 ETTPPKYLHYDEETSHQLLDCDCKPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLDCDCKPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIFCLKHSRCPGPGVGVQAGTPERNTV 120
DB 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIFCLKHSRCPGPGVGVQAGTPERNTV 120
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSSEQOTFOLLKWKHQH 240
DB 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSSEQOTFOLLKWKHQH 240
QY 241 KAQDIVKKIIQDIDLCEVSRQHIQHANTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
DB 241 KAQDIVKKIIQDIDLCEVSRQHIQHANTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
QY 301 SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 301 SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 361 QKLFLEMIGNOVQSVKISCL 380

RESULT 2
US-10-676-358-1
; Sequence 1, Application US/10676358
; Publication No. US20040137074A1
; GENERAL INFORMATION:
; APPLICANT: Nestec SA
; TITLE OF INVENTION: Osteoprotegerin in Milk
; FILE REFERENCE: 88265-6852
; CURRENT APPLICATION NUMBER: US/10/676,358
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: WO 2002 EP 02912
; PRIOR FILING DATE: 2003-03-15
; PRIOR APPLICATION NUMBER: EP 20010108414
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 380
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-676-358-1

Query Match 100.0%; Score 2085; DB 16; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.9e-167; Indels 0; Gaps 0;
Matches 380; Conservative 0; Mismatches 0;

QY 1 ETTPPKYLHYDEETSHQLLDCDCKPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLDCDCKPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIFCLKHSRCPGPGVGVQAGTPERNTV 120
DB 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIFCLKHSRCPGPGVGVQAGTPERNTV 120
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSSEQOTFOLLKWKHQH 240

DB 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSSEQOTFOLLKWKHQH 240
QY 241 KAQDIVKKIIQDIDLCEVSRQHIQHANTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
DB 241 KAQDIVKKIIQDIDLCEVSRQHIQHANTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
QY 301 SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 301 SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 361 QKLFLEMIGNOVQSVKISCL 380

RESULT 3
US-10-142-658-2
; Sequence 2, Application US/10142658
; Publication No. US20030022834A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Scatena, Marta
; APPLICANT: Giachelli, Cecilia M.
; TITLE OF INVENTION: METHODS AND DEVICES FOR PROMOTING ENDOTHELIAL MORPHOGENESIS
; FILE REFERENCE: UMOT1118975
; CURRENT APPLICATION NUMBER: US/10/142,658
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: US 60/290,230
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-142-658-2

Query Match 100.0%; Score 2085; DB 14; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.1e-167; Indels 0; Gaps 0;
Matches 380; Conservative 0; Mismatches 0;

QY 1 ETTPPKYLHYDEETSHQLLDCDCKPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 21 ETTPPKYLHYDEETSHQLLDCDCKPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 80
QY 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIFCLKHSRCPGPGVGVQAGTPERNTV 120
DB 81 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIFCLKHSRCPGPGVGVQAGTPERNTV 140
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
DB 141 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 200
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSSEQOTFOLLKWKHQH 240
DB 201 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSSEQOTFOLLKWKHQH 260
QY 241 KAQDIVKKIIQDIDLCEVSRQHIQHANTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
DB 261 KAQDIVKKIIQDIDLCEVSRQHIQHANTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 320
QY 301 SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 321 SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 380
QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 381 QKLFLEMIGNOVQSVKISCL 400

RESULT 4
US-09-405-032-125

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; Sequence 125, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-09-405-032-125

Query Match 100.0%; Score 2085; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPHYHYTDSWHTSDECL 60
DB 22 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPHYHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 120
DB 82 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 240
DB 202 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 261
QY 241 KAQDIVKKLIQIDILCENSQVRHIGHANLTFEQLRSLMESLPCKKVGABEDIEKTIKACP 300
DB 262 KAQDIVKKLIQIDILCENSQVRHIGHANLTFEQLRSLMESLPCKKVGABEDIEKTIKACP 321
QY 301 SQIILKLSLWRKNGDQDTLKLGMALHAKSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SQIILKLSLWRKNGDQDTLKLGMALHAKSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLFMIGNQVQSVKISCL 380
DB 382 QKLFLFMIGNQVQSVKISCL 401

RESULT 5
US-10-151-071-8
; Sequence 8, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William

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; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-071-8

Query Match 100.0%; Score 2085; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPHYHYTDSWHTSDECL 60
DB 22 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPHYHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 120
DB 82 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 240
DB 202 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 261
QY 241 KAQDIVKKLIQIDILCENSQVRHIGHANLTFEQLRSLMESLPCKKVGABEDIEKTIKACP 300
DB 262 KAQDIVKKLIQIDILCENSQVRHIGHANLTFEQLRSLMESLPCKKVGABEDIEKTIKACP 321
QY 301 SQIILKLSLWRKNGDQDTLKLGMALHAKSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SQIILKLSLWRKNGDQDTLKLGMALHAKSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLFMIGNQVQSVKISCL 380
DB 382 QKLFLFMIGNQVQSVKISCL 401

RESULT 6
US-10-467-243-2
; Sequence 2, Application US/10467243
; Publication No. US20040132971A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.
; APPLICANT: Haaning, Jesper Mortensen
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 0226w0310
; CURRENT APPLICATION NUMBER: US/10/467,243
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: DK PA 2001 00214
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00498
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/278,320
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-467-243-2

Query Match 100.0%; Score 2085; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETFFPKYLHDEETSHQLLDCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFFPKYLHDEETSHQLLDCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
Qy 61 YCSPVCKELQVVKQECNTHNRVCECKGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 120
Db 82 YCSPVCKELQVVKQECNTHNRVCECKGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 141
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 201
Qy 181 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABSVRIKROHSSQOQTFOQLLKLWKHQN 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABSVRIKROHSSQOQTFOQLLKLWKHQN 261
Qy 241 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
Qy 301 SDQILKLLSLWRINKNGDQDTLKGMLHALKHSKTYHFPKTVTOSLKKTIIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRINKNGDQDTLKGMLHALKHSKTYHFPKTVTOSLKKTIIRFLHSFTMYKLY 381
Qy 361 QKLFLEMIGNQVQSVKISL 380
Db 382 QKLFLEMIGNQVQSVKISL 401

RESULT 7

US-10-676-358-6

; Sequence 6, Application US/10676358

; Publication No. US20040137074A1

; GENERAL INFORMATION:

; APPLICANT: Nestec SA

; TITLE OF INVENTION: Osteoprotegerin in Milk

; FILE REFERENCE: 88265-6852

; CURRENT APPLICATION NUMBER: US/10/676,358

; PRIOR FILING DATE: 2003-10-02

; PRIOR APPLICATION NUMBER: WO 2002 EP 02912

; PRIOR FILING DATE: 2003-03-15

; PRIOR APPLICATION NUMBER: EP 20010108414

; PRIOR FILING DATE: 2001-04-03

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 537

; TYPE: PRT

; ORGANISM: artificial

; FEATURE:

; OTHER INFORMATION: protein sequence including mature OPG

US-10-676-358-6

Query Match

Best Local Similarity 100.0%; Score 2085; DB 16; Length 537;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETFFPKYLHDEETSHQLLDCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

Db 158 ETFFPKYLHDEETSHQLLDCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 217

Qy 61 YCSPVCKELQVVKQECNTHNRVCECKGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 120

Db 218 YCSPVCKELQVVKQECNTHNRVCECKGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 277

Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180

Db 278 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 337
Qy 181 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABSVRIKROHSSQOQTFOQLLKLWKHQN 240
Db 338 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABSVRIKROHSSQOQTFOQLLKLWKHQN 397
Qy 241 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 398 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 457
Qy 301 SDQILKLLSLWRINKNGDQDTLKGMLHALKHSKTYHFPKTVTOSLKKTIIRFLHSFTMYKLY 360
Db 458 SDQILKLLSLWRINKNGDQDTLKGMLHALKHSKTYHFPKTVTOSLKKTIIRFLHSFTMYKLY 517
Qy 361 QKLFLEMIGNQVQSVKISL 380
Db 518 QKLFLEMIGNQVQSVKISL 537

RESULT 8

US-09-062-113-4

; Sequence 4, Application US/09062113

; Patent No. US20020051969A1

; GENERAL INFORMATION:

; APPLICANT: GOTO, Masaaki

; APPLICANT: TSUDA, Eisuke

; APPLICANT: MOCHIZUKI, Shin'ichi

; APPLICANT: YANO, Kazuki

; APPLICANT: KOBAYASHI, Fumie

; APPLICANT: SHIMA, No. US20020051969A1uuyuki

; APPLICANT: YASUDA, Hisataka

; APPLICANT: NAKAGAWA, No. US20020051969A1uaki

; APPLICANT: MORINAGA, Tomonori

; APPLICANT: UEDA, Masatsugu

; APPLICANT: HIGASHIO, Kanji

; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing

; TITLE OF INVENTION: the Proteins

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Testa, Hurwitz & Thibault

; STREET: 125 High St.

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/062,113

; FILING DATE: 17-APR-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 54977/1995

; FILING DATE: 20-FEB-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 207508/1995

; FILING DATE: 21-JUL-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP96/00374

; FILING DATE: 20-FEB-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,004

; FILING DATE: 20-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MOORE, Ronda P.

; REGISTRATION NUMBER: 44,244

; REFERENCE/DOCKET NUMBER: FJN-060DV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 380 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..380
 ; OTHER INFORMATION: /note= "(OCIF protein without
 ; OTHER INFORMATION: signal peptide)"
 US-09-062-113-4

Query Match 99.7%; Score 2079; DB 9; Length 380;
 Best Local Similarity 99.7%; Pred. No. 9.4e-167;
 Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ETFPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 Db 1 ETFPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVKELQYVQKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVVQAGTPERTV 120
 Db 61 YCSPVKELQYVQKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVVQAGTPERTV 120
 QY 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
 Db 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
 QY 181 CEAFPRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOBTQFQLKLWKHQN 240
 Db 181 CEAFPRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOBTQFQLKLWKHQN 240
 QY 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 Db 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 QY 301 SQQILKLLSLWRKNGDQDTLKLHMLKHSKTYHFPKTVTQSLKKTIRFLHSFTWKLY 360
 Db 301 SQQILKLLSLWRKNGDQDTLKLHMLKHSKTYHFPKTVTQSLKKTIRFLHSFTWKLY 360
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 9

US-10-232-858-4
 ; Sequence 4, Application US/10232858
 ; Publication No. US20030153048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOTO, Masaaki
 ; APPLICANT: TSUDA, Eisuke
 ; APPLICANT: MOCHIZUKI, Shin'ichi
 ; APPLICANT: YANO, Kazuki
 ; APPLICANT: KOBAYASHI, Fumie
 ; APPLICANT: SHIWA, No. US20030153048A1uyuki
 ; APPLICANT: YASUDA, Hisataka
 ; APPLICANT: NAKAGAWA, No. US20030153048A1uaki
 ; APPLICANT: MORINAGA, Tomonori
 ; APPLICANT: UEDA, Masatsugu
 ; APPLICANT: HIGASHIO, Kanji
 ; TITLE OF INVENTION: No. US20030153048A1el Proteins and Methods for Producing the Pro
 ; FILE REFERENCE: 16991.004
 ; CURRENT APPLICATION NUMBER: US/10/232,858
 ; CURRENT FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: PCT/JP96/00374
 ; PRIOR FILING DATE: 1996-02-20
 ; PRIOR APPLICATION NUMBER: 08/915,004
 ; PRIOR FILING DATE: 1997-08-20
 ; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 380
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-232-858-4

Query Match 99.7%; Score 2079; DB 14; Length 380;
 Best Local Similarity 99.7%; Pred. No. 9.4e-167;
 Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ETFPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 Db 1 ETFPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVKELQYVQKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVVQAGTPERTV 120
 Db 61 YCSPVKELQYVQKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVVQAGTPERTV 120
 QY 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
 Db 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
 QY 181 CEAFPRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOBTQFQLKLWKHQN 240
 Db 181 CEAFPRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOBTQFQLKLWKHQN 240
 QY 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 Db 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 QY 301 SQQILKLLSLWRKNGDQDTLKLHMLKHSKTYHFPKTVTQSLKKTIRFLHSFTWKLY 360
 Db 301 SQQILKLLSLWRKNGDQDTLKLHMLKHSKTYHFPKTVTQSLKKTIRFLHSFTWKLY 360
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 10

US-10-785-109-4
 ; Sequence 4, Application US/10785109
 ; Publication No. US20040142426A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOTO, Masaaki
 ; APPLICANT: TSUDA, Eisuke
 ; APPLICANT: MOCHIZUKI, Shin'ichi
 ; APPLICANT: YANO, Kazuki
 ; APPLICANT: KOBAYASHI, Fumie
 ; APPLICANT: SHIWA, Nobuyuki
 ; APPLICANT: YASUDA, Hisataka
 ; APPLICANT: NAKAGAWA, Nobuaki
 ; APPLICANT: MORINAGA, Tomonori
 ; APPLICANT: UEDA, Masatsugu
 ; APPLICANT: HIGASHIO, Kanji
 ; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
 ; FILE REFERENCE: 16991.017
 ; CURRENT APPLICATION NUMBER: US/10/785,109
 ; CURRENT FILING DATE: 2004-02-25
 ; PRIOR APPLICATION NUMBER: US 10/232,858
 ; PRIOR FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: US 08/915,004
 ; PRIOR FILING DATE: 1997-08-20
 ; PRIOR APPLICATION NUMBER: PCT/JP96/00374
 ; PRIOR FILING DATE: 1996-02-20
 ; PRIOR APPLICATION NUMBER: JP 207508/1995
 ; PRIOR FILING DATE: 1995-07-21
 ; PRIOR APPLICATION NUMBER: JP 054977/1995
 ; PRIOR FILING DATE: 1995-02-20
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4

Tue Nov 16 08:10:28 2004

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; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-109-4

Query Match          99.7%; Score 2079; DB 16; Length 380;
Best Local Similarity 99.7%; Pred. No. 9.4e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYHSDMHTSDECL 60
Db 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYHSDMHTSDECL 60
QY 61 YCSPVCKELQVQKOECHNRTHRVCECKEGRYLEIFCLKHRSCTPPGCVQAGTPERNIV 120
Db 61 YCSPVCKELQVQKOECHNRTHRVCECKEGRYLEIFCLKHRSCTPPGCVQAGTPERNIV 120
QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
Db 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
QY 241 KAQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDETEKTKACKP 300
Db 241 KDQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDETEKTKACKP 300
QY 301 SDQILKLLSLWRKNGDQDTLKLGMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 301 SDQILKLLSLWRKNGDQDTLKLGMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
QY 361 QKLFLEMIGNQVQSVKISCL 380
Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 11
US-10-785-114-4
; Sequence 4, Application US/10785114
; Publication No. US20040143859A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, Nobuaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
; FILE REFERENCE: 16991.016
; CURRENT APPLICATION NUMBER: US/10785,114
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004
; PRIOR FILING DATE: 1997-08-20
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: JP 207508/1995
; PRIOR FILING DATE: 1995-07-21
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 380
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-785-114-4

Query Match          99.7%; Score 2079; DB 16; Length 380;
Best Local Similarity 99.7%; Pred. No. 9.4e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYHSDMHTSDECL 60
Db 1 ETTPPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKWKTVCAPCPDHYHSDMHTSDECL 60
QY 61 YCSPVCKELQVQKOECHNRTHRVCECKEGRYLEIFCLKHRSCTPPGCVQAGTPERNIV 120
Db 61 YCSPVCKELQVQKOECHNRTHRVCECKEGRYLEIFCLKHRSCTPPGCVQAGTPERNIV 120
QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
Db 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
QY 241 KAQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDETEKTKACKP 300
Db 241 KDQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDETEKTKACKP 300
QY 301 SDQILKLLSLWRKNGDQDTLKLGMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 301 SDQILKLLSLWRKNGDQDTLKLGMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
QY 361 QKLFLEMIGNQVQSVKISCL 380
Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 12
US-09-062-113-106
; Sequence 106, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
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; FILING DATE: 20-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: FJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-062-113-106

Query Match 99.7%; Score 2079; DB 9; Length 391;
Best Local Similarity 99.7%; Pred. No. 9.7e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	60
DB	12	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	71
QY	61	YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV	120
DB	72	YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV	131
QY	121	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	180
DB	132	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	191
QY	181	CBEAFPRFAPVPTFTNWLVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	240
DB	192	CBEAFPRFAPVPTFTNWLVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	251
QY	241	KAQDIVKKLIQDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	300
DB	252	KQDIVKKLIQDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	311
QY	301	SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHPKVTQSLKKTIRFLHSFTMYKLY	360
DB	312	SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHPKVTQSLKKTIRFLHSFTMYKLY	371
QY	361	QKLFLEMIGNQVQSVKISCL	380
DB	372	QKLFLEMIGNQVQSVKISCL	391

RESULT 13

US-10-232-858-106
; Sequence 106, Application US/10232858
; Publication No. US20030153048A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20030153048A1uyuki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu

; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20030153048A1el Proteins and Methods for Producing the Prote
; FILE REFERENCE: 16991.004
; CURRENT APPLICATION NUMBER: US/10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: 08/915,004
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-232-858-106

Query Match 99.7%; Score 2079; DB 14; Length 391;
Best Local Similarity 99.7%; Pred. No. 9.7e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	60
DB	12	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	71
QY	61	YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV	120
DB	72	YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVGVQAGTPERTV	131
QY	121	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	180
DB	132	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	191
QY	181	CBEAFPRFAPVPTFTNWLVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	240
DB	192	CBEAFPRFAPVPTFTNWLVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	251
QY	241	KAQDIVKKLIQDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	300
DB	252	KQDIVKKLIQDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	311
QY	301	SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHPKVTQSLKKTIRFLHSFTMYKLY	360
DB	312	SDQILKLLSLWRKNGDQDTLKGMLHAKHSKTYHPKVTQSLKKTIRFLHSFTMYKLY	371
QY	361	QKLFLEMIGNQVQSVKISCL	380
DB	372	QKLFLEMIGNQVQSVKISCL	391

RESULT 14

US-10-785-109-106
; Sequence 106, Application US/10785109
; Publication No. US20040142426A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, Nobuaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
; CURRENT APPLICATION NUMBER: US/10/785,109
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004

A;Cross-references: UNIPROT:P25119; GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R;Goodwin, K.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
 A;Reference number: A40254; MUID:91246168; PMID:1645445
 A;Accession: A40254
 A;Molecule type: mRNA
 A;Residues: 1-474 <GO>
 A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R;Kisnerghis, M.; Fellows, R.; Feldmann, M.; Chernajovskiy, Y.
 submitted to the EMBL Data Library, May 1995
 A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A;Reference number: S54816
 A;Accession: S54816
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-22 <KIS>
 A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C;Keywords: cytokine receptor; transmembrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F;40-77/Domain: NGF receptor repeat homology <NG1>
 F;79-120/Domain: NGF receptor repeat homology <NG2>
 F;166-203/Domain: NGF receptor repeat homology <NG4>
 Query Match 16.0%; Score 333.5; DB 2; Length 474;
 Best Local Similarity 35.7%; Pred. No. 2.8e-15;
 Matches 74; Conservative 23; Mismatches 85; Indels 25; Gaps 6;
 QY 9 HYDETSHLLCDKCPGGYLYKHCHTAKWTCAPCPDHYHYSWHTSDCLYCSFVCKE 68
 DB 46 YDRA--QMCCKAPPGQYVHFNCISDTVCACEASWYQVWQNFCTCLSCSSCTT 103
 QY 69 LQYVQECNRTHNRVCEKEGRYLEIF-----CLKHRSPPGFGVVQAGTPERNVVC 121
 DB 104 DQVEIRACTKQNRVCAACEAGYCALKTHSGSCRCMLSKGCPGFGVASSRAPNGVLC 163
 QY 122 KCPDGGFSNETSSKAPCRKHNCVFGILLQKGNATHNLCSGNSESTQKCGIDVTLIC 181
 DB 164 KACAPGTFSDTSTSDVCSPHRCISFLAI-----PGNAVDAVCA--PESFTLSAIPRTU- 216
 QY 182 BEAFFRFAVPTKFTENWLSVLVDNLPG 208
 DB 217 ---YVSQPEPTRSQP-----LDQEPG 234
 RESULT 3
 A35356
 tumor necrosis factor receptor 2 precursor [validated] - human
 N;Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
 C;Species: Homo sapiens (man)
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C;Accession: A35356; A48416; A36007; A23666; B35010; I38094
 R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K
 Science 248, 1019-1023, 1990
 A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
 A;Reference number: A35356; MUID:90260639; PMID:2160731
 A;Accession: A35356
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-461 <SWI>
 A;Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA5929.1; PID:g189186
 R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A;Reference number: A36475; MUID:91045991; PMID:2172983
 A;Accession: A36475
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-195, 'R', 197-461 <KOH>
 A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.

Cytokine 2, 231-237, 1990
 A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A;Reference number: A48416; MUID:91370690; PMID:1966549
 A;Accession: A48416
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 23-461 <DEM>
 A;Cross-references: GB:S63368; NID:g235648; PIDN:AA19824.1; PID:g235649
 A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)
 R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
 A;Reference number: A36007; MUID:90349572; PMID:2166946
 A;Accession: A36007
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
 A;Cross-references: GB:M55857; NID:g339751; PIDN:AA63262.1; PID:g339752
 R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
 J. Biol. Chem. 265, 20131-20138, 1990
 A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A;Reference number: A23666; MUID:91056048; PMID:2173696
 A;Accession: A23666
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 23-40;65-69;136-141;300-306 <LOE>
 R;Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A;Reference number: A35010; MUID:90110215; PMID:2153136
 A;Accession: B35010
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 27-31 <ENG>
 R;Kuhnert, P.; Kemper, O.; Wallach, D.
 Gene 150, 381-386, 1994
 A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A;Reference number: I38094; MUID:95121934; PMID:7821811
 A;Accession: I38094
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-37 <RES>
 A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 C;Genetics:
 A;Gene: GDB:TNFR2
 A;Cross-references: GDB:125914; OMIM:191191
 A;Map position: 1p36.2-1p36.2
 A;Introns: 26/3
 A;Note: the list of introns is incomplete
 C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F;40-76/Domain: NGF receptor repeat homology <NG1>
 F;78-119/Domain: NGF receptor repeat homology <NG2>
 F;120-162/Domain: NGF receptor repeat homology <NG3>
 F;164-201/Domain: NGF receptor repeat homology <NG4>
 F;262-279/Domain: transmembrane #status predicted <TMN>
 F;280-461/Domain: intracellular #status predicted <INT>
 F;171.193/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 15.8%; Score 330; DB 1; Length 461;
 Best Local Similarity 39.8%; Pred. No. 4.7e-15;
 Matches 66; Conservative 16; Mismatches 72; Indels 12; Gaps 3;
 QY 9 HYDETSHLLCDKCPGGYLYKHCHTAKWTCAPCPDHYHYSWHTSDCLYCSFVCKE 68
 DB 45 YDQ--TAQMCCSKSPGQAKVFCRTSDTVCDSCESTYITQLWNVPECLSGSRCS 102
 QY 69 LQYVQECNRTHNRVCEKEGRYLEI-----BFLKHSRCPGFGVVQAGTPERNVVC 122
 DB 103 DQVEIRACTKQNRVCAACEAGYCALKTHSGSCRCMLSKGCPGFGVASSRAPNGVVC 162

C:Genetics:

A:Gene: G4R
 C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
 F:32-66/Domain: NGF receptor repeat homology <NGF>
 F:68-109/Domain: NGF receptor repeat homology <NG2>
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 11.2%; Score 232.5; DB 2; Length 349;

Best Local Similarity 23.6%; Pred. No. 1.4e-08;

Matches 89; Conservative 47; Mismatches 158; Indels 83; Gaps 14;

QY 4 PPKYLHYDEE-TSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCPDHYVYDTSWHTSDCLYC 62

Db 27 PPNKCKKDETEYKRNLCCLSCPPGTASRLCDSTNTQCTPCGSGTFTSRNNHLPACLSC 86

QY 63 SPVCKELQYVKQECNRTHNVCKEGRYLEI-----EFLKHSRCPGPGVWQAGTPE 116

Db 87 NGRCSNQVETRSCNTHNRICESPYYCLLKGSGCKACVQTKGIGYG-VSGHTSV 145

QY 117 RNTVCKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTQGNATHDNIC-----SGNSEST 171

Db 146 GDVLCSPCGGTYSHTVSSADKCEPVNNTFNIDVILYVPNDTSCRTTITGLSESI 205

QY 172 QKCGIDVTLL-----CEAFAFPRAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSQE 227

Db 206 LTSBELATITMNHDTCPNVF-----RE 225

QY 228 QTFOLLK-----LWKHONKAQDIVKKIQQIDIDLCEMSVQRHIGHANLTFEOLRLMESL 281

Db 226 EYFSLVKVATSGFFTGGENRYQNLK-----VCTLNFBIKCNKNGSGSPKQUTKAKND- 277

QY 282 PGKVGGAEDIETIKA-CKPSDQILKLLSLWRINKGQDQTLKGLMHALKHKSXTYHFP--- 337

Db 278 DGMMSHSETV--TLAGDCLSSVDIYILYNTNAQDYETDISYRVGNVLDLDDDS-HMPGSC 334

QY 338 ---KTVTQSLUKTIRFL 351

Db 335 NIHKPITNS--KPTRFL 349

RESULT 10

D72175

G2R protein - variola minor virus (strain Garcia-1966)

C:Species: variola minor virus

C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004

C:Accession: D72175

R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar

submitted to Genbank, March 1998

A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor

A:Reference number: A72150

A:Accession: D72175

A:Molecule type: DNA

A:Residues: 1-349 <SHC>

A:Cross-references: UNIPROT:P34015; GB:X16780; NID:g5830555; PIDN:CAB54798.1; PID:g58307

A:Experimental source: strain Garcia-1966

C:Genetics:

A:Gene: G2R

C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 11.0%; Score 229.5; DB 2; Length 349;

Best Local Similarity 23.6%; Pred. No. 2.3e-08;

Matches 89; Conservative 46; Mismatches 159; Indels 83; Gaps 14;

QY 4 PPKYLHYDEE-TSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCPDHYVYDTSWHTSDCLYC 62

Db 27 PPNKCKKDETEYKRNLCCLSCPPGTASRLCDSTNTQCTPCGSGTFTSRNNHLPACLSC 86

QY 63 SPVCKELQYVKQECNRTHNVCKEGRYLEI-----EFLKHSRCPGPGVWQAGTPE 116

Db 87 NGRCSNQVETRSCNTHNRICESPYYCLLKGSGCKACVQTKGIGYG-VSGHTSV 145

QY 117 RNTVCKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTQGNATHDNIC-----SGNSEST 171

Db 146 GDVLCSPCGGTYSHTVSSADKCEPVNNTFNIDVILYVPNDTSCRTTITGLSESI 205

QY 172 QKCGIDVTLL-----CEAFAFPRAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRQHSQE 227

Db 206 LTSBELATITMNHDTCPNVF-----RE 225

QY 228 QTFOLLK-----LWKHONKAQDIVKKIQQIDIDLCEMSVQRHIGHANLTFEOLRLMESL 281

Db 226 EYFSLVKVATSGFFTGGENRYQNLK-----VCTLNFBIKCNKNGSGSPKQUTKAKND- 277

QY 282 PGKVGGAEDIETIKA-CKPSDQILKLLSLWRINKGQDQTLKGLMHALKHKSXTYHFP--- 337

Db 278 DGMMSHSETV--TLAGDCLSSVDIYILYNTNAQDYETDISYRVGNVLDLDDDS-HMPGSC 334

QY 338 ---KTVTQSLUKTIRFL 351

Db 335 DIHKLITNS--KPTRFL 349

RESULT 11

B43692

T2 protein - rabbit fibroma virus

C:Species: rabbit fibroma virus, Shope fibroma virus

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: B43692

R:Upton, C.; DeLange, A.M.; McFadden, G.

A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A:Reference number: A43692; MUID:87321103; PMID:2820128

A:Accession: B43692

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-325 <UPT>

A:Cross-references: UNIPROT:P25943; GB:M17433

C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

F:64-105/Domain: NGF receptor repeat homology <NG2>

F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 10.8%; Score 225; DB 2; Length 325;

Best Local Similarity 30.9%; Pred. No. 4.3e-08;

Matches 55; Conservative 22; Mismatches 89; Indels 12; Gaps 4;

QY 18 LLCDKCPGTYLKQHTAKWKTVCAPCPDHYVYDTSWHTSDCLYCSPVCKELQYVKQECN 77

Db 38 LCACSHPGFYASRLCGPSGNTVCSPECDGTFTASTNHAPACVSCRCGCTGHLSESQPCD 97

QY 78 RTHNRVCECKEGRYLEI-----FCLKHSRCPGPGVWQAGTPERNTVCKRCPDGFFSN 131

Db 98 RTHDRVNCSTGNYCLLKQNGCRICAPQTKCPAGYG-VSGHTRAGDTLCEKCPHTYSD 156

QY 132 ETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQKCGIDVTLL-----CEBAF 185

Db 157 SLSPTEKCGTSFNYSVGNL-YPVNETSCTTAGHNEVIKTEFTVILNYTDCDPVF 213

RESULT 12

GOVZML

T2 protein - myxoma virus (strain Lausanne)

C:Species: myxoma virus

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: A40566

R:Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.

A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis fa

A:Reference number: A40566; MUID:91335768; PMID:1651597

A:Molecule type: DNA

A:Residues: 1-326 <UPT>

A:Cross-references: UNIPROT:P29825; GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; I

C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

F:64-105/Domain: NGF receptor repeat homology <NG2>


```
RESULT 15
GQRTT1
tumor necrosis factor receptor 1 precursor - rat
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: B36555
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: B36555
A:Molecule type: mRNA
A:Residues: 1-461 <HIM>
A:Cross-references: UNIPROT:P22934; GB:M63122; NID:g207361; PID:AAA42256.1; PID:g207362
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:44-82/Domain: tumor necrosis factor binding protein #status predicted <TBP>
F:84-126/Domain: NGF receptor repeat homology <NG1>
F:127-167/Domain: NGF receptor repeat homology <NG2>
F:168-204/Domain: NGF receptor repeat homology <NG3>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-461/Domain: intracellular #status predicted <INT>
F:54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      8.9%; Score 185; DB 1; Length 461;
Best Local Similarity 20.9%; Pred. No. 3.3e-05;
Matches 89; Conservative 47; Mismatches 116; Indels 174; Gaps 21;

QY      6 KYLHYDEETSHQLCKCPGTVLKQHTAK-WKTVCAPCPDHYVYDTSWHTSDECLYCSP 64
Db      ||| :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: |||
48 KYAH---PKNNSICTCKKHGTYLVSDCPSPGQGTVEVCVCKGTFTASQNHVRQCLSKT 104

QY      65 VCKELQVVK-QECNRTHNRYCECKEG--RYL-EIEF-CLKHRSCTPGF-GVVQAGTPER 117
Db      ||| :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: |||
105 CRKEMEQVEISPCADMVTCGCKKQFQRYLSETHFQCV---DCSPCFNGTIVTIPCKEK 161

QY      118 -NTVKRCRCPDGF--SNETSskapCRKHTNCVSFGLLLTKGNATHDN----- 162
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 QNTVC-NCHAGFTLSGNECTPCSHCKKQEC--MKLCPPVANVTNPQDSGTAVLLPLVI 218

QY      163 -----ICSGNSESTQ-----K 173
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
219 FLGLCLLFFICISLLCRYPQWRPRVYSIIICRDSAPKVEGEGIVTKPLTPASIPAFSPN 278

QY      174 CGIDVTLCBAAPFAVPTKFTP-----NW----- 198
Db      ||| :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: |||
279 PGFNPTLGFSTTFRSHFVSSFTISPVFGPSNWHNFVPVREVVTQGDPLLYGSLNPV 338

QY      199 -----LSVLVDNLFGTK-----VNAESVERIKEQ 222
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
339 PIPAPVRKWDVVAAQFQRLDTADPAMLYAVVDGVPPTRWKEFMRLLGLSEHEIERLEIQ 398

QY      223 HSS--QEQTFFQLKLWKHKQKAO-----DIVKTIQIDL--CENSVORHIGHANLTFEOL 274
Db      :|: :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: ||| ||| :|: |||
399 NGRCLREAHYSMLEAWRRRTPRHEATLDVVGVLCDMLRGC-----LENI 444

QY      275 RSLMES 280
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
445 RETLES 450
```

Search completed: November 15, 2004, 19:01:13
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 18:38:30 / Search time 192 Seconds
(without alignments)
1138.762 Million cell updates/sec

Title: US-10-676-358-1

Perfect score: 2085

Sequence: 1 ETFFPKYLHYDEETSHQLLC.....QKLFLEMIGNQVQSVKISCL 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2079	99.7	401	1	TL1B HUMAN
2	1834	88.0	401	2	O6P1I2
3	1834	88.0	401	2	AHA49782
4	1828	87.7	401	1	TL1B RAT
5	1820	87.3	401	1	TL1B MOUSE
6	1028.5	49.3	387	2	O6GLN3
7	525	25.2	146	2	O7ZZY4
8	450	21.6	186	2	O7ZZY5
9	440.5	21.1	300	1	TR6B HUMAN
10	411.5	19.7	302	2	O9PU50
11	380.5	18.2	285	2	O90W71
12	372.5	17.9	285	2	O90Y56
13	365	17.5	286	2	O6NM61
14	365	17.5	286	2	AAH67712
15	337	16.2	268	2	O6YI29
16	337	16.2	268	2	AAH72434
17	336.5	16.1	459	2	O62327
18	333.5	16.0	474	1	TR1B MOUSE
19	333.5	16.0	474	2	BAB23533
20	333.5	16.0	474	2	BAB23610
21	330	15.8	461	1	TR1B HUMAN
22	328	15.7	482	2	O88734
23	322.5	15.5	433	2	O91ZM6
24	322.5	15.5	461	2	O6VAU8
25	322.5	15.5	461	2	AAQ22350
26	322.5	15.5	474	2	O80WY6
27	322.5	15.5	651	1	O9ASM6
28	302.5	14.5	655	1	TR21 HUMAN
29	302.5	14.5	655	2	AAH36088
30	298	14.3	483	2	O800K7
31	297	14.2	457	2	O81VS6

32	297	14.2	457	2	AAH11844
33	293	14.1	655	1	TR21 MOUSE
34	293	14.1	655	2	BAC31664
35	284.5	13.6	289	1	TNR5 MOUSE
36	284.5	13.6	289	2	O8K2X6
37	284.5	13.6	289	2	BAC40978
38	279.5	13.4	467	2	O800I0
39	270	12.9	467	2	O9JKE0
40	267	12.8	169	2	O8SQ34
41	267	12.8	462	2	O805B0
42	265	12.7	276	2	O9DDD2
43	264	12.7	223	2	O86YK5
44	264	12.7	277	1	TNR5 HUMAN
45	257	12.3	318	2	O7T2H3

Aah11844 homo sapi
Q8epus mus musculu
Bac31664 mus muscu
P27512 mus musculu
O8k2x6 mus musculu
Bac40978 mus muscu
Q800i0 gallus gall
Q9jke0 rattus norv
Q8sq34 sus scrofa
Q805b0 gallus gall
Q9ddd2 gallus gall
O86yK5 homo sapien
P25942 homo sapien
Q7t2h3 oncornynchu

ALIGNMENTS

RESULT 1

TL1B HUMAN

ID TL1B HUMAN STANDARD; PRT; 401 AA.

AC O00300; O60236; Q9UHP4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 11B precursor

DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).

GN Name=TNFRSF11B; Synonyms=OPG, OCIF;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=97262071; PubMed=9108485;

RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,

Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,

Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,

Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,

Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,

Suggs S., Boyle W.J.;

"Osteoprotegerin: a novel secreted protein involved in the regulation

of bone density.";

Cell 89:309-319(1997).

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung cancer;

RX MEDLINE=98151033; PubMed=9492069;

RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,

Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,

Tsuda E., Morinaga T., Higashio K.;

"Identity of osteoclastogenesis inhibitory factor (OCIF) and

osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits

osteoclastogenesis in vitro.";

Endocrinology 139:1329-1337(1998).

[3]

RP SEQUENCE FROM N.A., AND VARIANT ASN-3.

RC TISSUE=Placenta;

RX MEDLINE=98351569; PubMed=9688283;

RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;

"Cloning and characterization of the gene encoding human

osteoprotegerin/osteoclastogenesis-inhibitory factor.";

Eur. J. Biochem. 254:685-691(1998).

[4]

RP SEQUENCE FROM N.A., AND VARIANTS ASN-3 AND MET-104.

RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,

Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,

Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;

"NIHES-SNPs, environmental genome project, NIHES ES15478, Department

of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";

Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

[5]
SEQUENCE FROM N.A., AND VARIANT ASN-3.
RT TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[6]
PP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159; DOI=10.1006/bbr.1998.8443;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor.";
RL Biochem. Biophys. Res. Commun. 245:382-387 (1998).
[7]
PP SEQUENCE OF 22-36.
RA Zhang Z., Henzel W.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Submitted (JUN-2004) to Swiss-Prot.
[8]
PP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL Acta Biochim. Biophys. Sin. 31:680-684 (1999).
[9]
PP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977; DOI=10.1006/bbr.1997.6603;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 234:137-142 (1997).
[10]
PP TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 273:14363-14367 (1998).
[11]
PP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.;
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor.";
RL J. Biol. Chem. 273:5117-5123 (1998).
[12]
PP REVIEW.
RX MEDLINE=21395914; PubMed=11505389;
RX DOI=10.1002/1097-0142(20010801)22:3<450::AID-CNCR1344>3.0.CO;2-D;
RA Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases.";
RL Cancer 92:460-470 (2001).
[13]
PP VARIANT JPD ASP-182 DEL.
RX PubMed=12189164;
RA Cundy T., Hegde M., Naot D., Chong B., King A., Wallace R., Mulley J.,
RA Love D.R., Seidel J., Pawlner M., Banovic T., Callon K.E., Grey A.B.,
RA Reid I.R., Middleton-Hardie C.A., Cornish J.;
RT "A mutation in the gene TNFRSF11B encoding osteoprotegerin causes an
RT idiopathic hyperphosphatasia phenotype.";
RL Hum. Mol. Genet. 11:2119-2127 (2002).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC lymph node, trachea, adrenal gland, testis, and bone marrow.
CC Detected at very low levels in brain, placenta and skeletal
CC muscle. Highly expressed in fetal kidney, liver and lung.
CC -!- INDUCTION: Up-regulated by increasing calcium-concentration in the
CC medium and estrogens. Down-regulated by glucocorticoids.
CC -!- PTM: N-glycosylated. Contains sialic acid residues.
CC -!- PTM: The N-terminus is blocked.
CC -!- DISEASE: Defects in TNFRSF11B are the cause of juvenile Paget
CC disease (JPD) (MIM:239000); also called hyperostosis corticalis
CC deformans juvenilis or hereditary hyperphosphatasia or chronic
CC congenital idiopathic hyperphosphatasia. JPD is a rare autosomal
CC recessive osteopathy that presents in infancy or early childhood.
CC The disorder is characterized by rapidly remodeling woven bone,
CC osteopenia, debilitating fractures, and deformities due to a
CC markedly accelerated rate of bone remodeling throughout the
CC skeleton. Approximately 40 cases of JPD have been reported
CC worldwide. Unless it is treated with drugs that block osteoclast-
CC mediated skeletal resorption, the disease can be fatal.
CC -!- SIMILARITY: Contains 2 death domains.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U94332; AAB53709.1; -;
CC EMBL: AB002146; BAA55910.1; -;
CC EMBL: AB008822; BAA32076.1; -;
CC EMBL: AB008821; BAA32076.1; JOINED.
CC EMBL: AY466112; AAR23265.1; -;
CC EMBL: BC030155; AAH30155.1; -;
CC EMBL: AF134187; AAF20168.1; -;
CC HSP: Q14783; IDOG.
CC Genew: HGNC:11909; TNFRSF11B.
CC MIM: 602643; -;
CC MIM: 239000; -;
CC GO: GO:0005576; C:extracellular; TAS.
CC GO: GO:0003125; F:cytokine activity; TAS.
CC GO: GO:0004872; F:receptor activity; TAS.
CC GO: GO:0007165; P:signal transduction; TAS.
CC GO: GO:0001501; P:skeletal development; TAS.
CC InterPro: IPR000488; Death.
CC InterPro: IPR011029; DEATH like.
CC InterPro: IPR009030; Growth_Fac_recept.
CC InterPro: IPR001368; TNFR_C5.

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DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SMO0005; DEATH; 1.

Query Match
Best Local Similarity 99.7%; Score 2079; DB 1; Length 401;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQCHTAKWTKVACPCPDHYTDSWHTSDECL 60
DB 22 ETFPKYLHYDEETSHQLLCKCPGTYLKQCHTAKWTKVACPCPDHYTDSWHTSDECL 81

QY 61 YCSPVKELQVVKQECNRTNHRVCEKGRYLEFELFKHRSKCPGPGVQAGTPERTV 120
DB 82 YCSPVKELQVVKQECNRTNHRVCEKGRYLEFELFKHRSKCPGPGVQAGTPERTV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCIDVT 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCIDVT 201

QY 181 CEEAFFRAVPTKFTFNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 240
DB 202 CEEAFFRAVPTKFTFNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 261

QY 241 KAQDIVKKIIQDIDLCEVSVQRHGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACKP 300
DB 262 KQDQIVKKIIQDIDLCEVSVQRHGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACKP 321

QY 301 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLFMIGNQVQSVKISCL 380
DB 382 QKLFLFMIGNQVQSVKISCL 401

RESULT 2
Q6P112 PRELIMINARY; PRT; 401 AA.
AC Q6P112;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 11b
DE (Osteoprotegerin).
GN Name=tnfrsf11b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Limb;
RA Strausberg R.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049782; AAH49782.1; -
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR GO; GO:0042489; P:negative regulation of ontogenesis (sensu. .; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR Pfam; PF00020; TNFR_C6; 4-
DR SMART; SMO0005; DEATH; 1.
DR PROSITE; PS00208; TNFR; 4.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 401 AA; 45965 MW; 7C708B52EB46BA0E CRC64;

Query Match 88.0%; Score 1834; DB 2; Length 401;
Best Local Similarity 86.6%; Pred. No. 2.3e-122;
Matches 329; Conservative 25; Mismatches 26; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKCPGTYLKQCHTAKWTKVACPCPDHYTDSWHTSDECL 60
DB 22 ETFPKYLHYDEETSHQLLCKCPGTYLKQCHTAKWTKVACPCPDHYTDSWHTSDECL 81

QY 61 YCSPVKELQVVKQECNRTNHRVCEKGRYLEFELFKHRSKCPGPGVQAGTPERTV 120
DB 82 YCSPVKELQVVKQECNRTNHRVCEKGRYLEFELFKHRSKCPGPGVQAGTPERTV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCIDVT 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCIDVT 201

QY 181 CEEAFFRAVPTKFTFNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 240
DB 202 CEEAFFRAVPTKFTFNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 261

QY 241 KAQDIVKKIIQDIDLCEVSVQRHGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACKP 300
DB 262 KQDQIVKKIIQDIDLCEVSVQRHGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACKP 321

QY 301 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLFMIGNQVQSVKISCL 380
DB 382 QKLFLFMIGNQVQSVKISCL 401

RESULT 3
AAH49782 PRELIMINARY; PRT; 401 AA.
ID AAH49782;
AC AAH49782;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 11b
DE (Osteoprotegerin).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
```


RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.O., Lu X., Gibbs R.A., Schenz A.,
RA Fahy J., Helton E., Kettner M., Madan A.C., Rodriguez S., Rodriguez S.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinchwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
PP SEQUENCE FROM N.A.
RC TISSUB=Lmb;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049782; AHA49782.1; -.
KW Receptor.
SQ SEQUENCE 401 AA; 45965 MW; 7C708B52EB46BA0E CRC64;
Query Match 88.0%; Score 1834; DB 2; Length 401;
Best Local Similarity 86.6%; Pred. No. 2.3e-122;
Matches 329; Conservative 25; Mismatches 26; Indels 0; Gaps 0;
QY 1 ETPFKYLYHDETSQHLCDKCPGTYLKQCTAKWTVCAPCPDHYVTSWHTSDECL 60
DB 22 ETLPKYLYHDETSQHLCDKCPGTYLKQCTAKWTVCAPCPDHYVTSWHTSDECV 81
QY 61 YGSPVCKELQYVQECNTHNRVCEKRGYLEIEFCLKHRSCTPGFVGWQAGTPEINTV 120
DB 82 YGSPVCKELQYVQECNTHNRVCEKRGYLEIEFCLKHRSCTPGFVGWQAGTPEINTV 141
QY 121 CKRCPDGFNSSTKAPCKRHTNCSVGLLLITQGNATHNICSGNSESTQKCGIDVTL 180
DB 142 CKKCPDGFNSSTKAPCKRHTNCSVGLLLITQGNATHNICSGNSESTQKCGIDVTL 201
QY 181 CEAEFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRHSOEOFTQKLLWKQON 240
DB 202 CEAEFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRHSOEOFTQKLLWKQON 261
QY 241 KAQDVIKKIIQIDICENSQVRHIGHANLTFFQLRSLMESLPKGVGADIEKTIKACKP 300
DB 262 RDOENVKKIIQIDICENSQVRHIGHANLTFFQLRSLMESLPKGVGADIEKTIKACKP 321
QY 301 SQOILKLSLWRKNGQDQTLKGLMHALKHSKTYHFKTQSLKKTIRFLHSFTMYKLY 360
DB 322 SEQLLKLSLWRKNGQDQTLKGLMHALKHSKTYHFKTQSLKKTIRFLHSFTMYRUY 381
QY 361 QKLFLEMIGNQVSKISCL 380
DB 382 QKLFLEMIGNQVSKISCL 401
RESULT 4
ID T11B RAT STANDARD; PRT; 401 AA.
AC 008727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN Name=TNFRsf1b; Synonyms=Opg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUB=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Durst C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density."
RL Cell 89:309-319 (1997).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Up-regulated by osteopontin.
CC -!- SIMILARITY: Contains 2 death domains.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U94330; AB553707.1; -.
DR HSP; P19438; INCF.
DR RGD; 619802; Tnfrsf1b.
DR InterPro; IPR00488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR009030; Growth_recept.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; 2.
DR Apoptosis; Cytokine; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 21 By similarity.
FT CHAIN 22 401 Tumor necrosis factor receptor
FT superfamily member 11B.
FT REPEAT 24 62 TNFR-Cys 1.
FT REPEAT 65 105 TNFR-Cys 2.
FT REPEAT 107 142 TNFR-Cys 3.
FT REPEAT 145 185 TNFR-Cys 4.
FT DOMAIN 198 269 Death 1.
FT DOMAIN 270 365 Death 2.
FT SITE 400 400 Involved in dimerization (By similarity).
FT DISULFID 41 54 By similarity.
FT DISULFID 44 62 By similarity.
FT DISULFID 65 80 By similarity.
FT DISULFID 83 97 By similarity.
FT DISULFID 87 105 By similarity.
FT DISULFID 107 118 By similarity.
FT DISULFID 124 142 By similarity.
FT DISULFID 145 160 By similarity.
FT DISULFID 166 185 By similarity.
FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 401 AA; 46192 MW; FECA31F1D4E573A CRC64;

Query Match 87.7%; Score 1828; DB 1; Length 401;
 Best Local Similarity 86.3%; Pred. No. 6.2e-122;
 Matches 328; Conservative 24; Mismatches 28; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKDPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 22 ETFPKYLHYDEETSHQLLCKDPPGYLKHQCTAKWKTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVCKELQVKECNRTNHRVCEKGRVLETFGLKHSRCPGPGVQAGTPERTV 120
 DB 82 YCSPVCKELQVKECNRTNHRVCEKGRVLETFGLKHSRCPGPGVQAGTPERTV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNICGENSESTQKGIQDVTL 180
 DB 142 CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNICGENSESTQKGIQDVTL 201

QY 181 CBAFFRAFPVPTKTPNWLSDVNLPGTKVNAESVERIKRHSQBOQTQLLKLWKHQN 240
 DB 202 CBAFFRAFPVPTKTPNWLSDVNLPGTKVNAESVERIKRHSQBOQTQLLKLWKHQN 261

QY 241 KAQDIKVLITQDIDLCESSVORHGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
 DB 262 RQEMWKKLITQDIDLCESSVORHGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 321

QY 301 SDQILKLSLWRIKNGDQTLKGLMHAKHSKTVHFPTVTSQTKTIRFLHSFTWYKLY 360
 DB 322 SEQLLKLSLWRIKNGDQTLKGLMHAKHSKTVHFPTVTSQTKTIRFLHSFTWYKLY 381

QY 361 QKLFLEMIGNQVQSVKISCL 380
 DB 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 5

TL1B_MOUSE
 ID TL1B_MOUSE STANDARD; PRT; 401 AA.
 AC 008712; 070202;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 GN Name=TNfrs1b; Synonyms=OPG, OCIF;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Kidney;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehly R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
 RP AND ARG-296.
 RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
 RX MEDLINE=98382527; PubMed=9714833;
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda E., Morinaga T.,
 RA Higashio K.;
 RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
 RT gene and its expression in embryogenesis.";
 RL Gene 215:339-343(1998).
 RN [3]
 RP FUNCTION.

RX MEDLINE=21060987; PubMed=10952716;
 RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
 RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
 RA Simonet W.S.;
 RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
 RT osteoclasts and prevents vascular calcification by blocking a process
 RT resembling osteoclastogenesis.";
 RL J. Exp. Med. 192:463-474(2000).
 CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
 CC intestines and calvaria. Highly expressed in decidua and placenta,
 CC and in embryo.
 CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
 CC whereas expression decreases at day 11 and increases from day 15
 CC to 17. On day 15 found in developing bone primordia,
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,
 CC abdominal aorta and midgut.
 CC -!- INDUCTION: Up-regulated by TGF-beta and estrogens. Down-regulated
 CC by 1,25-dihydroxyvitamin D3 and parathyroid hormone.
 CC -!- SIMILARITY: Contains 2 death domains.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 CC EMBL: U94331; AAB53708.1; -;
 CC EMBL: AB013898; BAA28269.1; -;
 CC EMBL: AB013903; BAA33388.1; -;
 CC EMBL: AB013899; BAA33388.1; JOINED.
 CC EMBL: AB013900; BAA33388.1; JOINED.
 CC EMBL: AB013901; BAA33388.1; JOINED.
 CC EMBL: AB013902; BAA33388.1; JOINED.
 CC HSSP: OI4763; ID0G.
 CC MGD: MGI:109587; Tnfrs1b.
 CC GO: GO:0005578; C:extracellular matrix; IDA.
 CC InterPro: IPR000488; Death.
 CC InterPro: IPR011029; DEATH like.
 CC InterPro: IPR009030; Grow_fac_recept.
 CC InterPro: IPR001368; TNFR_c6.
 CC Pfam: PF00020; TNFR_c6; 3.
 CC SMART: SM00005; DEATH; 1.
 CC SMART: SM00208; TNFR; 4.
 CC PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC PROSITE: PS00852; TNFR_NGFR_1; 1.
 CC PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC Apoptosis; Glycoprotein; Polymorphism; Receptor; Repeat; Signal.
 FT SIGNAL 1 21 By similarity.
 FT CHAIN 22 401 Tumor necrosis factor receptor
 FT superfamily member 11B.
 FT REPEAT 24 62 TNFR-Cys 1.
 FT REPEAT 65 105 TNFR-Cys 2.
 FT REPEAT 107 142 TNFR-Cys 3.
 FT REPEAT 145 185 TNFR-Cys 4.
 FT DOMAIN 198 269 Death 1.
 FT DOMAIN 283 365 Death 2.
 FT SITE 400 400 Involved in dimerization (By similarity).
 FT DISULFID 41 54 By similarity.
 FT DISULFID 44 62 By similarity.
 FT DISULFID 65 80 By similarity.
 FT DISULFID 83 97 By similarity.

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FT DISULFID 87 105 By similarity.
FT DISULFID 107 118 By similarity.
FT DISULFID 124 142 By similarity.
FT DISULFID 145 160 By similarity.
FT DISULFID 166 185 By similarity.
FT CARBOHYD 98 98 N-linked (GlcNAc... ) (potential).
FT CARBOHYD 165 165 N-linked (GlcNAc... ) (potential).
FT CARBOHYD 178 178 N-linked (GlcNAc... ) (potential).
FT CARBOHYD 289 289 N-linked (GlcNAc... ) (potential).
FT VARIANT 138 138 R -> P (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 161 161 I -> R (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 165 165 N -> D (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 288 288 S -> A (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 296 296 L -> R (in strain 129/Ola and strain NIH Swiss).
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 87.3%; Score 1820; DB 1; Length 401;
Best Local Similarity 86.1%; Pred. No. 2.3e-121;
Matches 327; Conservative 25; Mismatches 28; Indels 0; Gaps 0;

QY 1 ETEPPKYLHYDEETSHQLLCKDKCPGTYLKQHTAKWTKVCAPCPDHYTDSWHTSDECL 60
DB 22 ETLPPKYLHYDEETSHQLLCKDKCAPGTYLKQHTVRRKTLVCPCPDHYTDSWHTSDECV 81

QY 61 YCSPVKELQVYKQECNTHNRVCEKEGRYLEIFCLKHSRSCPPGFGVQAGTPERNTV 120
DB 82 YCSPVKELQVYKQECNTHNRVCEKEGRYLEIFCLKHSRSCPPGFGVQAGTPERNTV 141

QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKCGIDVTYL 180
DB 142 CKKCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKCGIDVTYL 201

QY 181 CBEAFRAVPTKFTPNMLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQN 240
DB 202 CBEAFRAVPTKFTPNMLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQN 261

QY 241 KAQDIVKKIQQIDILCENSQVORHIGHANLTFQLSLMESLPGKKVGAEDIEKTKACKXP 300
DB 262 RQEMVKKIQQIDILCENSQVORHIGHANLTFQLLKLWKHQN 321

QY 301 SDQILKLWLRIKNGDQDTLKGMLHAKHSKTYHFPKTVTOSLKTIRFLHSFTWYKLY 360
DB 322 SEQLLKLWLRIKNGDQDTLKGMLHAKHSKTYHFPKTVTOSLKTIRFLHSFTWYKLY 381

QY 361 QKLFLEMIGNQVQSVKISCL 380
DB 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 6
Q6GLN3
ID Q6GLN3 PRELIMINARY; PRT; 387 AA.
AC Q6GLN3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Boraudo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Kaba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P., Harte S., Garcia A.M., Guy L.J., Hulyk S.W.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RN Dev. Dyn. 225:384-391(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074428; AAH74428.1; -.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00552; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Hypothetical protein.
SQ SEQUENCE 387 AA; 44568 MW; F365C364A11484AA CRC64;

Query Match 49.3%; Score 1028.5; DB 2; Length 387;
Best Local Similarity 48.7%; Pred. No. 4.7e-65;
Matches 182; Conservative 68; Mismatches 111; Indels 13; Gaps 5;

QY 4 PKYLYHDEETSHQLLCKDKCPGTYLKQHTAKWTKVCAPCPDHYTDSWHTSDECLYCS 63
DB 24 PKYSHYDPTSMYLCQDCHCPGTYLKQDCKTEKTECAPCSHHVNDKNSNTEQFCN 83

QY 64 PVCKELQVYKQECNTHNRVCEKEGRYLEIFCLKHSRSCPPGFGVQAGTPERNTVCKR 123
DB 84 VVCKELQVYKQECNTHNRVCEKEGRYLEIFCLKHSRSCPPGFGVQAGTPESDTCRP 143

QY 124 CPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKCGIDVTLCSE 183
DB 144 CPEGTFSDSTSATRCQKHTDCKKLGIVAYQGDSDHDTLCOPEGSF---CEIDITLCOE 200

QY 184 AFREFAVPTKFTPNMLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQNAQ 243
DB 201 AFREFV-VPN---NMLTAIAFPSTWSSQVIEGVQEKRDQEHAFHLFLKWKHNRES 255

QY 244 DIVKKIQQIDILCENSQVORHIGHANLTFQLSLMESLPGKKVGAEDIEKTKACKXPQ 303
DB 256 ESGKHLFDQLQVCEKVKVSKHIGLNVTATQATLTKSLPFGNKISKRELETTVKICRQDPQ 315

QY 304 ILKLSLWLRIKNGDQDTLKGMLHAKHSKTYHFPKTVTOSLKTIRFLHSFTWYKLYQKL 363
DB 316 VLKLSLWLRIKNGG-DTI-----NLLKVTIKTNLRKMRRTIKKLEQFLNSDENRYLYQKL 370

QY 364 FLEMIGNQVQSVKI 377

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Db 371 LLEIFGSOQPAKV 384

RESULT 7
Q7ZZY4 PRELIMINARY; PRT; 146 AA.
AC Q7ZZY4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Osteoprotegerin (Fragment).
GN Name=OPG;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22760275; PubMed=12878204;
RA Bridgman J.T., Johnson A.L.;
RT "Characterization of chicken TNFR superfamily decoy receptors, DcR3
and osteoprotegerin."; Commun. 307:956-961(2003).
RL Biochem. Biophys. Res. Commun. 307:956-961(2003).
DR EMBL; AY251407; AAP03890.1; -.
GO: GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac_recept.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON TER 146
SQ SEQUENCE 146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;

Query Match 25.2%; Score 525; DB 2; Length 146;
Best Local Similarity 69.7%; Pred. No. 1e-29;
Matches 85; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 4 PPXYLYHDEETSHQLLCKDPCPPGYLKQHTAKWKVCAPCPDHYTDSWHTSDECLYCS 63
Db 25 PPXYLYHDEETSHQLLCKDPCPPGYLKQHTAKWKVCAPCPDHYTDSWHTSDECLYCS 84
NCBI_TaxID=9031;

QY 64 PVCKELQYVQKQCNRTNRYCECKEGRYLEIFCLKHSRCPGPGVYVQAGTPERNTVCKR 123
Db 85 AVCKELQYIKQETSTQDRVCECLIGWYLEIFCLKHTCCPPGPGVYVQAGTPERNTVCKR 144
NCBI_TaxID=9031;

QY 124 CP 125
Db 145 CP 146

RESULT 8
Q7ZZY5 PRELIMINARY; PRT; 186 AA.
AC Q7ZZY5;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Decoy receptor 3 (Fragment).
GN Name=DcR3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22760275; PubMed=12878204;
RA Bridgman J.T., Johnson A.L.;
RT "Characterization of chicken TNFR superfamily decoy receptors, DcR3

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and osteoprotegerin."; Commun. 307:956-961(2003).
RL Biochem. Biophys. Res. Commun. 307:956-961(2003).
DR EMBL; AY251406; AAP03889.1; -.
GO: GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac_recept.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON TER 186
SQ SEQUENCE 186 AA; 20671 MW; 31D65731DACB758E CRC64;

Query Match 21.6%; Score 450; DB 2; Length 186;
Best Local Similarity 48.7%; Pred. No. 3e-24;
Matches 75; Conservative 24; Mismatches 55; Indels 0; Gaps 0;

QY 4 PPXYLYHDEETSHQLLCKDPCPPGYLKQHTAKWKVCAPCPDHYTDSWHTSDECLYCS 63
Db 32 PPTYQWRDAGTKERVTCCQPPGTFVAQHCTKERPTVCAPCPDLHYTHYNNYLEKLYCN 91
NCBI_TaxID=9031;

QY 64 PVCKELQYVQKQCNRTNRYCECKEGRYLEIFCLKHSRCPGPGVYVQAGTPERNTVCKR 123
Db 92 VXGERQVEVQQCNATHNRACQCEQFHAEMEFVQHSEXXPGSGVYVKGSPSENTQCR 151
NCBI_TaxID=9031;

QY 124 CPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGN 157
Db 152 CPRGFSFSSSSSTPCRAHQNCCTQLGKENTVPGN 185
NCBI_TaxID=9031;

RESULT 9
TR6B HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68)
UNQ186/PRO312).
GN Name=TNFRSF6B; Synonyms=DcR3, TR6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
colon cancer."
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGM-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;

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RT "Overexpression of M68/DcR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen B., Chow B., Chui C., Crowley C., Currell B., Duell B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wian D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment";
RL Genome Res. 13:2265-2270 (2003).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blake S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.B., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Vaudin M., Wall M., Wallis J.M.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871 (2001).
RN [6]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung, and Skin;
RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-1- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT
and TNFSF6/PASL. Protects against apoptosis.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
Detected in adult stomach, spinal cord, lymph node, trachea,
spleen, colon and lung. Highly expressed in several primary tumors
from colon, stomach, rectum, esophagus and in SW480 colon
carcinoma cells.
-1- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL; AF104419; AAD03056.1; -
EMBL; AF134240; AAD29688.1; -
EMBL; AF217796; AAF35244.1; -
EMBL; AF217793; AAF33685.1; -
EMBL; AF217794; AAF33686.1; -
EMBL; AY358279; AAQ88646.1; -
EMBL; AL121845; CAC03668.1; -
EMBL; BC017065; AAH17065.1; -
EMBL; BC034349; AAH34349.1; -
HSSP; O14763; 1DU3.
Genew; HGNC:11921; TNFRSF6B.
MIM; 603361; -
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0006916; P:anti-apoptosis; TAS.
InterPro; IPR009030; Grow_fac_recept.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR 1; 1.
PROSITE; PS00500; TNFR_NGFR 2; 2.
Apoptosis; Direct protein sequencing; Glycoprotein; Receptor; Repeat;
Signal.
CHAIN 1 29
Tumor necrosis factor receptor
superfamily member 6B.
REPEAT 31 70
TNFR-Cys 1.
REPEAT 72 113
TNFR-Cys 2.
REPEAT 115 150
TNFR-Cys 3.
REPEAT 152 193
TNFR-Cys 4.
By similarity.
DISULFID 49 62
By similarity.
DISULFID 52 70
By similarity.
DISULFID 73 88
By similarity.
DISULFID 91 105
By similarity.
DISULFID 115 126
By similarity.
DISULFID 132 150
By similarity.
DISULFID 153 168
By similarity.
DISULFID 174 193
By similarity.
FT CARBOHYD 173 173
N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

Query Match 21.1%; Score 440.5; DB 1; Length 300;
Best Local Similarity 41.2%; Pred. No. 2.5e-23;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 BKLVHDETSHLLCDKCPGTYLKHCHTAKWKTVCAPCPHYITDSWHTSDECLYCSP 64
Db 34 PTYPRDAETGERLVCAQCPPTGTVQVPCRRSPITCGCPRHYYTFQWYLERCRYCNV 93
QY 65 VKELQYVQECNRTHNRVCECKEGRYLIEFLKHSRSCFPGGVQVQAGTPERTVCKRC 124
Db 94 LCGEREERARACHATHNACRCKRTGFFAHAGFCLHSCPPGAGVIAPTGPTSQOCPC 153

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QY 125 PDGFFNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNBESTQKCGIDVTLC 181
Db 154 PPGTFSSASSSSQCPHRNCTALGALNVPGSSSHDLTCTGTFPLSTVRPGAER--C 211

QY 182 REAFFRF 198
Db 212 ERAVIDF 218

RESULT 10
Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation."
RL Biol. Reprod. 62:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 19.7%; Score 411.5; DB 2; Length 302;
Best Local Similarity 32.0%; Pred. No. 2.9e-21;
Matches 96; Conservative 57; Mismatches 110; Indels 37; Gaps 9;

QY 11 DRETSQLLCDKCPPTGTYLKQHTAKWKTVCAPCPDHYTDSMHTSDECLYCSVCKELQ 70
Db 27 DRYSGLSIVCDRCPPGTLYLRAPCSAMRKSDCAPCPNGAVTEFWNHLSKLCRCS-MCAENQ 85

QY 71 YVQECNRTHNRVCECKEGRYL--EIEFCLKHSRCPGFGVQAGTPERTNTVCKRCPDGF 128
Db 86 VVQKCSPPNCECECKEGYFNKYACIKHKECPGPGANTGPHODTECVQCAQF 145

QY 129 FSNETSAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTLCCEAFFRF 188
Db 146 YSEVSSAKATCLAQSNCKVGLRVLLKGDWENTLSCSYDLKTRDGE-----YLIE 198

QY 189 AVPTKFTPNWLSVLDNLEPGTKNAESVERIKRQSHSSQGTQLLKLWKHQNKAQDIVKK 248
Db 199 ILPTFTF-----IQLHQTGMIKMRRLAMRLPQEGGKPLIGAVMK--RNRRLGHDFM-- 248

QY 249 IIOIDILCNSVQRHGHANLTFEQLRSIMESI;PGKKVGAEDI-EKTIKACKPSDILKL 307
Db 249 -----NSWDQAGN-----DQVKLPEVL--RKIGAFNMGDKLERKLAIDQQSKL 292

RESULT 11
Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Pleguezuelos O., Secombes C.J.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ315137; CAC43329.1; -.
DR HSSP; O14763; 1D0G.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF 2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;

Query Match 18.2%; Score 380.5; DB 2; Length 285;
Best Local Similarity 38.1%; Pred. No. 4.3e-19;
Matches 74; Conservative 25; Mismatches 88; Indels 7; Gaps 3;

QY 5 PKYLHYDEBTSHOLLCDKCPPTGTYLKQHTAKWKTVCAPCPDHYTDSMHTSDECLYCS 64
Db 29 FTYIWRDDATGSLTCDLCAPGTYLLKHCTDKRSDCGPCPKSHYTEIWNVIERCQYCN 88

QY 65 VKELQVYQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNTVCKRC 124
Db 89 FCTADIESVPTQLHNRQCECKDGFYTHGSCSRHRRCPGEGVISNGTAHTDVKCEPC 148

QY 125 PDGFFNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSG--NSESTQKCGIDVTLC 182
Db 149 PVGFFSAVSSRRKACQKFSVCPGG--TTIPGNDMDNVYCSACTNGSRTHE---GEAICD 203

QY 183 EAFFRFVPTKTP 196
Db 204 GELMEFLSLQILT 217

RESULT 12
Q90YS6 PRELIMINARY; PRT; 285 AA.
AC Q90YS6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE TNF decoy receptor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21883732; PubMed=11886174;
RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT fragments containing AU-rich elements."
RL Cytokine 17:71-81(2002).
DR EMBL; AF401631; AAK91758.1; -.
DR HSSP; O14763; 1D0G.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.

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RL	Submitted (MAR-2004) to the EMBL/GenBank/DBDJ databases.	
DR	EMBL: BC067712; AAH67712.1; -	
DR	InterPro: IPR006209; EGF like.	
DR	InterPro: IPR001368; TNFR_c6.	
DR	Pfam: PF00020; TNFR_c6; 4.	
DR	SMART: SM00208; TNFR; 4.	
DR	PROSITE; PS01186; EGF_2; UNKNOWN 1.	
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1.	
DR	PROSITE; PS50050; TNFR_NGFR_2; 1.	
FT	NON_TER	1
SQ	SEQUENCE 286 AA; 32275 MW; 9P43CDC5FAC4E77B CRC64;	
	Query Match 17.5%; Score 365; DB 2; Length 286;	
	Best Local Similarity 32.4%; Pred.No. 5.5e-18;	
	Matches 89; Conservative 41; Mismatches 119; Indels 26; Gaps	
QY	7 YLHYDEETSHQLCDKCPGTYLKHQCTAKWKTVCAPCDPHYTDSDWHTSDDELYCSPVC	66
DB	18 YRKADPTGTLICARCAPGRLLRQHCSSRQTECSFGPGNYTFWNYIPDLCLCDS-C	76
QY	67 KELQYVQKQECNRTHNRVCEKGEYLIBEFCLKHRSPPGFGVQVQAGPENTVCKRCPD	126
DB	77 AEHQRVQPCNGIANTVCECEGEFYEQHFCRRHSVCRPGHGVKTAGTGYSDTVCEACAE	136
QY	127 GFPSNETSSKAPCEKHNTCSVFGILLTQKGNATHDNICGNSSESQKCGIDVTLCEEAFF	186
DB	137 GHFSDATKAHAQCVKHYRCQGEELL- -SGNTHNSICTTCQQLSNGGTVWTAFFDPLS	195
QY	187 RFAVPTKFTFNWLSVLVDNLPGTWNAESVBRIKQHSSEQBTFQLLKLWKH-QNKAAQDI	245
DB	196 ALQVQKIDIRHLEQMV- - - - -IRRLKK- - - - -FLKQLHKRTAMRADP	234
QY	246 VKKTIQIDLCENSQVRHIGHANTFTEQLRSLMES	280
DB	235 SEGLIDRSMLENTYLSHL- -AQRMTQNIIRVQOS	267
RESULT 14		
AAH67712	PRELIMINARY; PRT; 286 AA.	
AC	AAH67712;	
DT	24-MAY-2004 (TrEMBLrel. 27, Created)	
DT	24-MAY-2004 (TrEMBLrel. 27, Last sequence update)	
DT	24-MAY-2004 (TrEMBLrel. 27, Last annotation update)	
DE	LOC407674 protein (Fragment).	
GN	LOC407674.	
OS	Brachydanio rerio (zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RX	MEDLINE=22388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh P.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carlinici P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettaman M., Nadan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Nadan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.B., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.	
RT	"Generation and initial analysis of more than 15,000 full-length human	

